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Jenkinson et al.

(54) **UTILITY OF SNP MARKERS ASSOCIATED WITH MAJOR SOYBEAN PLANT MATURITY AND GROWTH HABIT GENOMIC REGIONS**

(76) Inventors: **Jonathan Jenkinson**, Ames, IA (US); **John Tamulonis**, Nevada, IA (US); **James Narvel**, Middletown, DE (US); **Kenneth Gruys**, Davis, CA (US); **Henry Valentin**, Davis, CA (US)

Correspondence Address:
ARNOLD & PORTER LLP
ATTN: IP DOCKETING DEPT.
555 TWELFTH STREET, N.W.
WASHINGTON, DC 20004-1206 (US)

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A01H 1/02	(2006.01)

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(57) **ABSTRACT**

The invention includes methods and compositions of genomic regions for screening and selecting plants and seeds from the genus *Glycine* associated with soybean plant maturity and growth habit. The invention also includes methods and compositions for screening plants and seeds from the genus *Glycine* with markers associated with genomic regions that are related to the plant maturity and plant growth habit of *Glycine* plants.

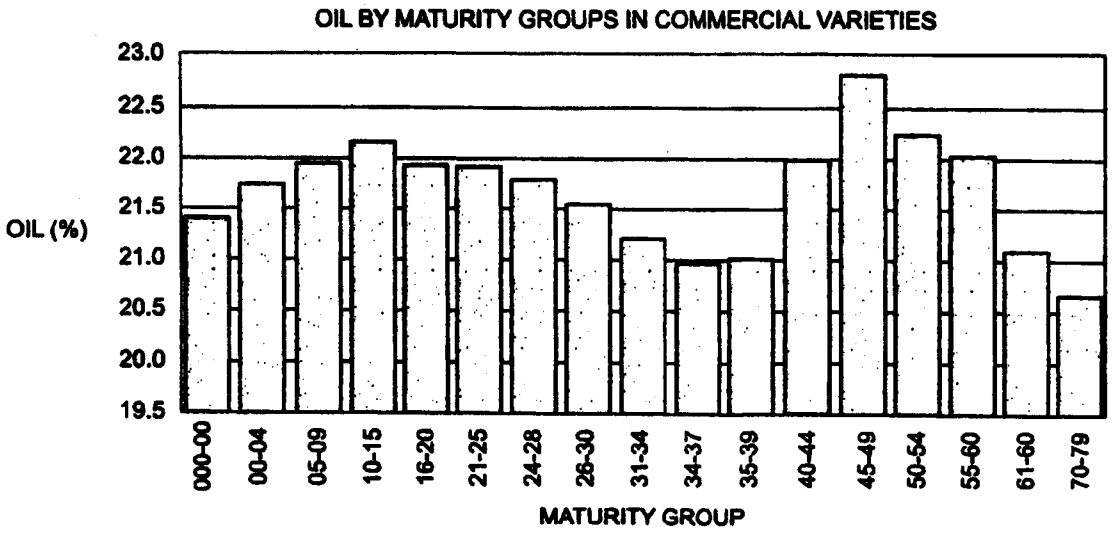
OIL BY MATURITY GROUPS IN COMMERCIAL VARIETIES
OIL (%)
23.0
22.5
22.0
21.5
21.0
20.5
20.0
19.5
000-00
00-04
05-09
10-15
16-20
21-25
24-28
26-30
31-34
34-37
35-39
40-44
45-49
50-54
55-60
61-60
70-79
MATURITY GROUP

FIG. 1

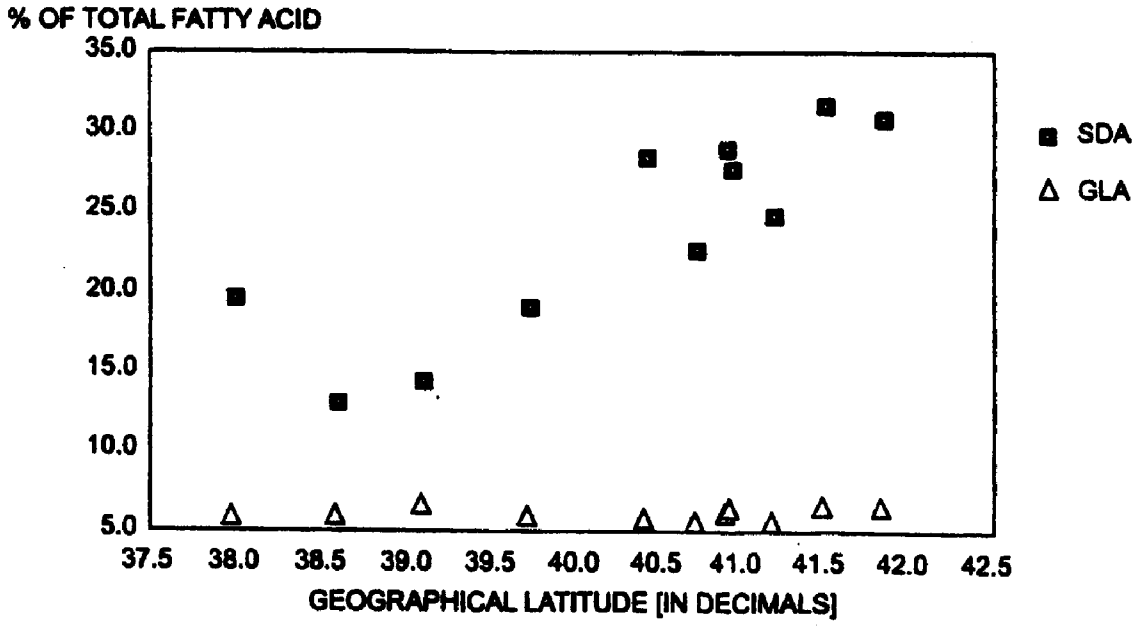
% OF TOTAL FATTY ACID
35.0
30.0
25.0
20.0
15.0
10.0
5.0
37.5
38.0
38.5
39.0
39.5
40.0
40.5
41.0
41.5
42.0
42.5
GEOGRAPHICAL LATITUDE [IN DECIMALS]
SDA
GLA

FIG. 2

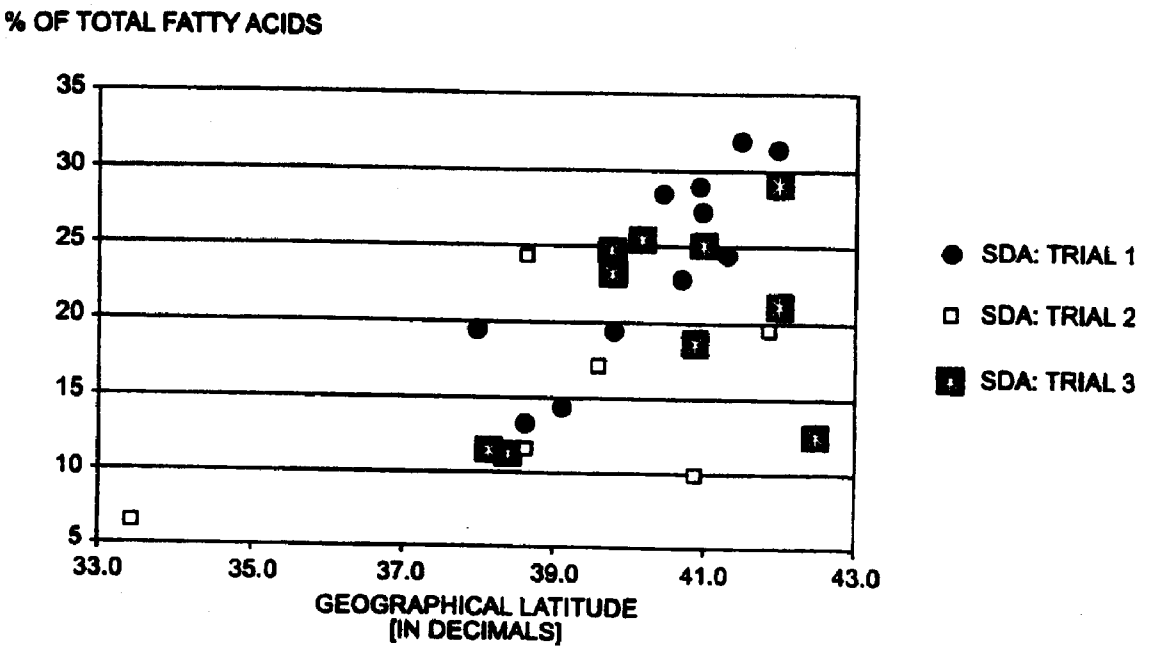
% OF TOTAL FATTY ACIDS
35
30
25
20
15
10
5
33.0
35.0
37.0
39.0
41.0
43.0
GEOGRAPHICAL LATITUDE
[IN DECIMALS]
SDA: TRIAL 1
SDA: TRIAL 2
SDA: TRIAL 3

FIG. 3

UTILITY OF SNP MARKERS ASSOCIATED WITH MAJOR SOYBEAN PLANT MATURITY AND GROWTH HABIT GENOMIC REGIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application Nos. 60/920,531, filed Mar. 28, 2007, and 61/001,049, filed Oct. 31, 2007. The entirety of each of these applications is hereby incorporated by reference.

INCORPORATION OF THE SEQUENCE LISTING

[0002] Two copies of the Sequence Listing and a computer readable form of the sequence listing on CD-ROM, each containing the file named "SequenceListing.txt", which is 140,000 bytes in size (measured in MS-Windows) are filed herewith and herein incorporated by reference. A paper copy of the Sequence Listing and a computer readable form of the sequence listing on diskette, containing the file named "pa_seq_54590.txt" which is 143,360 bytes in size (measured in MS-Windows) and which was recorded on Mar. 14, 2007 and filed in U.S. Application No. 60/920,531 are herein incorporated by reference.

FIELD OF THE INVENTION

[0003] The invention includes methods and compositions of genomic regions for screening and selecting plants and seeds from the genus *Glycine* associated with soybean plant maturity and growth habit. The invention also includes methods and compositions for screening plants and seeds from the genus *Glycine* with markers associated with genomic regions that are related to the plant maturity and plant growth habit of *Glycine* plants.

BACKGROUND OF THE INVENTION

[0004] The soybean, *Glycine max* (L.) Merril, is a major economic crop worldwide and is a primary source of vegetable oil and protein (Sinclair and Backman, *Compendium of Soybean Diseases,* 3rd Ed. APS Press, St. Paul, Minn., p. 106. (1989)). The growing demand for low cholesterol and high fiber diets has also increased importance of soybean as a health food.

[0005] Soybean varieties grown in the United States have a narrow genetic base. Six introductions, 'Mandarin,' 'Manchu,' 'Mandarin' (Ottawa), "Richland,' 'AK' (Harrow), and 'Mukden,' contributed nearly 70% of the germplasm represented in 136 cultivar releases. The genetic base of cultivated soybean could be widened through the use of exotic species. In addition, exotic species may possess such key traits as disease and stress resistance. At present, the traits of many exotic species are inaccessible in part due to limitations with crossing soybean plants from extremely different maturity groups. Most soybean variety development crosses are made between parents within 10 maturity days of each other. If the parents differ greatly in maturity, the progeny plants segregate widely for maturity. In order for breeders to obtain and select for soybean plants of the desired maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive.

[0006] Plant maturity and yield are closely associated in soybean. An increase of one day in maturity may be equivalent to a ~0.7 bu/A increase in yield. Conversely, a decrease in maturity is often penalized with a ~0.7 bu/A decrease in yield. The correlation of plant maturity and yield confounds the evaluation of potential quantitative trail loci (QTLs) and candidate genes associated with yield. The ability to genetically fix maturity within a soybean plant would be helpful and assist in elucidating traits associated with yield.

[0007] Soybean plants are short day plants, therefore flowering is initiated by short days due to a decrease in photoperiod (Garner & Allard, *J. Agric. Res.* 18, 553-606 (1920)). Consequently, photoperiod (day length) and temperature response of the soybean plant determine areas of plant adaptation. Due to photoperiod sensitivity, soybean genotypes are often grown in narrow zones of latitude to optimize yield. Northern soybean varieties, in contrast to Southern varieties, initiate flowering with longer days. Northern varieties planted south of their adaptation zone exhibit accelerated flowering, limited plant growth and reduced yield. Southern soybean varieties planted north of their adaptation zone will have delayed flowering with a potential for frost damage that may reduce yield.

[0008] Soybean plant varieties are classified based on bands of adaptation that are determined by latitude and day length. In North America, soybeans are categorized into 13 maturity groups with the designations ranging from maturity groups 000, 00, 0, and I through X. The earliest maturity group 000 soybeans are adapted to the north (45° latitude), while the latest maturity group X soybeans are adapted to regions near the equator. Soybean plants in maturity groups 000 to IV have indeterminate plant structure, while soybean plants in maturity groups V through X have determinate plant structure. Determinate varieties cease vegetative growth after the main stem terminates in a cluster of mature pods. Indeterminate varieties develop leaves and flowers simultaneously throughout a portion of their reproductive period, with one to three pods at the terminal apex. Early maturity varieties (000 to III) are adapted to northern latitudes with the maturity designation increasing in southern latitudes. The maturity group is determined by the maturity date. Plants are considered mature when 95% of the pods have reached their mature color. The maturity date is typically described as a measurement of days after August 31st in the northern hemisphere.

[0009] There is a need in the art of plant breeding to identify genomic regions associated with the maturity group of a soybean plant. At present, soybean breeders are limited to crossing plants within similar maturity groups. In addition, a number of traits, like oil levels, are influenced by latitude and maturity growing region. Therefore, there is a need for a rapid, cost-efficient method to pre-select for maturity group of soybean plants. The present invention includes a method for screening and selecting a soybean plant for a preferred plant maturity using single nucleotide polymorphism (SNP) technology.

BRIEF DESCRIPTION OF FIGURES

[0010] FIG. **1**: Influence of maturity group on percent oil in commercial soybeans.

[0011] FIG. **2**: Correlation of stearidonic acid (SDA) levels and GLA (gamma-linolenic acid) and latitude for mature soybean seeds. The soybean plants are transgenic and engineered to produce SDA and GLA.

[0012] FIG. **3**: Correlation of stearidonic acid (SDA) levels and latitude for mature soybean seeds over three trials. The soybean plants are transgenic and engineered to produce SDA.

SUMMARY OF THE INVENTION

[0013] The present invention includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1, 2, and 3; and assigning a maturity group value to the soybean plant or soybean seed.

[0014] In another aspect, the present invention includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1, 2, 3 and 4; and assigning a maturity group value to the soybean plant or soybean seed.

[0015] The present invention also includes a method of providing information about the maturity of a soybean plant or soybean seed by obtaining DNA from the soybean seed or soybean plant and determining the allelic profile at a locus of genomic region 4.

[0016] The present invention also includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and determining the allelic combination of the alleles within maturity genomic regions 1, 2, and 3.

[0017] An aspect of the present invention includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant by obtaining DNA from a soybean plant or soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1 and 2; and assigning a maturity growth value to the soybean plant or soybean seed.

[0018] In an aspect of the present invention, a method of soybean plant breeding includes crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group.

[0019] An aspect of the present invention includes a method of selecting a soybean plant for germplasm improvement by determining a maturity group by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group; and incorporating the selected soybean plant into a use selected from any of using the soybean plant for breeding, advancement of the soybean plant through self-fertilization, trait integration, use of soybean plant or parts thereof for transformation, and use of soybean plants or parts thereof for mutagenesis.

[0020] Another aspect of the present invention includes a method of co-selecting a soybean plant for expression of a non-maturity phenotypic trait and a maturity trait by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group; and determining the desired geography for the progeny soybean plant growth, and a method for determining the non-maturity phenotype.

[0021] In one aspect the present invention includes a method of soybean plant breeding by assaying a soybean plant for the presence of a marker sequences selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213; and associating the soybean plant with a maturity group.

[0022] In another aspect the present invention includes a method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent soybean plant, wherein the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days-20 days, or 10 days-30 days, by crossing a parent soybean plant comprising a desired trait with a second parent soybean plant; obtaining progeny soybean seed from the cross; screening a progeny soybean seed for the trait; screening a progeny soybean seed for a desired maturity group using a marker selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213 to determine the desired geographical growing region; and selecting a progeny soybean seed containing the desired trait and desired soybean plant maturity.

[0023] An aspect of the present invention includes a method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days-20 days, or days-30 days; obtaining a progeny soybean seed from the cross; genotyping a progeny soybean seed of the cross with a genetic marker; and selecting a soybean seed possessing a genotype for preferred maturity.

[0024] Another aspect of the present invention includes a method of screening soybean seeds based on soybean plant maturity group by obtaining DNA from a soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous;

determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and assigning a maturity growth value to the soybean seed.

[0025] One aspect of the present invention includes a method to select a soybean seed based on indeterminate or determinate growth habit comprising determining if maturity genomic region 3 is homozygous or heterozygous.

[0026] Another aspect of the present invention includes a method of distributing a soybean plant based on maturity group by obtaining DNA from a soybean plant; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and assigning a maturity growth value to the soybean plant; and shipping the soybean plant to a preferred geographic region.

[0027] Another aspect of the present invention includes a method to isolate indeterminate-early maturity soybean seeds by obtaining DNA from the soybean seed using a non-destructive method; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; and determining if an allele within maturity genomic region 2 is homozygous or heterozygous.

[0028] An aspect of the present invention includes a method of determining if a soybean seed will grow into a soybean plant having a maturity group of III-VI by determining a homozygous or heterozygous marker within the soybean seed using a marker with the nucleic acid sequence of SEQ ID NO: 151.

[0029] Another aspect of the present invention includes a method of determining if a soybean seed will grow into a soybean plant having a maturity group between 0.0-III.0 comprising determining if an 11-basepair insertion within the nucleic acid sequence of SEQ ID NO: 149 exists in the soybean seed.

[0030] An aspect of the present invention includes a method to determine if a soybean plant has a maturity group of 0.0-III.9 by determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; and assigning a maturity group value for the soybean plant between 0.0-III.9.

[0031] One aspect of the present invention is a method of introgressing an allele into a soybean plant by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; screening the progeny soybean plant of the cross for the allele; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; and selecting a soybean seed, wherein the soybean seed comprises the allele and a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-213.

[0032] Another aspect of the present invention includes a method of introducing a desired trait into a soybean plant by crossing at least two different parent soybean plants, wherein at least one parent soybean plant has a desired trait; obtaining a progeny soybean seed from the cross; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; assaying the progeny soybean seed of the cross for evidence of the desired trait; and selecting the soybean seed with the desired trait and a desired maturity group. In a preferred aspect, the desired trait is transgenic.

[0033] A further aspect of the present invention includes a method of introgressing an allele into a soybean plant by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; and selecting a soybean seed with the allele and a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-174.

[0034] A method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 10 days; obtaining progeny soybean seed from the cross; genotyping the progeny soybean seed of the cross with a genetic marker selected from the group consisting of SEQ ID NOs: 143-213; and selecting a soybean seed with a desired maturity group.

[0035] An aspect of the present invention includes a method of detecting maturity genomic region 4 by detecting an allele using a marker selected from any of SEQ ID NO: 175-180. Another aspect of the present invention includes a method of detecting maturity genomic region 5 by detecting an allele using a marker selected from any of SEQ ID NO: 181-189. Another aspect of the present invention includes a method of detecting maturity genomic region 6 by detecting an allele using a marker selected from any of SEQ ID NO: 190-196. Another aspect of the present invention includes a method of detecting maturity genomic region 7 by detecting an allele using a marker selected from any of SEQ ID NO: 197-203. Another aspect of the present invention includes a method of detecting maturity genomic region 8 by detecting an allele using a marker selected from any of SEQ ID NO: 204-213.

[0036] A further aspect of the present invention includes a soybean plant comprising within its genome an introgressed haplotype associated with maturity, wherein the introgression is facilitated by at least one of the markers from SEQ ID NO: 143-213.

Brief Description of Nucleic Acid Sequences

[0037] SEQ ID NO: 1 is a forward PCR primer for the amplification of SEQ ID NO: 143.

[0038] SEQ ID NO: 2 is a reverse PCR primer for the amplification of SEQ ID NO: 143.

[0039] SEQ ID NO: 3 is a forward PCR primer for the amplification of SEQ ID NO: 144.

[0040] SEQ ID NO: 4 is a reverse PCR primer for the amplification of SEQ ID NO: 144.

[0041] SEQ ID NO: 5 is a forward PCR primer for the amplification of SEQ ID NO: 145.

[0042] SEQ ID NO: 6 is a reverse PCR primer for the amplification of SEQ ID NO: 145.

[0043] SEQ ID NO: 7 is a forward PCR primer for the amplification of SEQ ID NO: 146.

[0044] SEQ ID NO: 8 is a reverse PCR primer for the amplification of SEQ ID NO: 146.

[0045] SEQ ID NO: 9 is a forward PCR primer for the amplification of SEQ ID NO: 147.

[0046] SEQ ID NO: 10 is a reverse PCR primer for the amplification of SEQ ID NO: 147.

[0047] SEQ ID NO: 11 is a forward PCR primer for the amplification of SEQ ID NO: 148.

[0048] SEQ ID NO: 12 is a reverse PCR primer for the amplification of SEQ ID NO: 148.

[0049] SEQ ID NO: 13 is a forward PCR primer for the amplification of SEQ ID NO: 149.

[0050] SEQ ID NO: 14 is a reverse PCR primer for the amplification of SEQ ID NO: 149.
[0051] SEQ ID NO: 15 is a forward PCR primer for the amplification of SEQ ID NO: 150.
[0052] SEQ ID NO: 16 is a reverse PCR primer for the amplification of SEQ ID NO: 150.
[0053] SEQ ID NO: 17 is a forward PCR primer for the amplification of SEQ ID NO: 151.
[0054] SEQ ID NO: 18 is a reverse PCR primer for the amplification of SEQ ID NO: 151.
[0055] SEQ ID NO: 19 is a forward PCR primer for the amplification of SEQ ID NO: 152.
[0056] SEQ ID NO: 20 is a reverse PCR primer for the amplification of SEQ ID NO: 152.
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[0064] SEQ ID NO: 28 is a reverse PCR primer for the amplification of SEQ ID NO: 156.
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[0067] SEQ ID NO: 31 is a forward PCR primer for the amplification of SEQ ID NO: 158.
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[0074] SEQ ID NO: 38 is a reverse PCR primer for the amplification of SEQ ID NO: 161.
[0075] SEQ ID NO: 39 is a forward PCR primer for the amplification of SEQ ID NO: 162.
[0076] SEQ ID NO: 40 is a reverse PCR primer for the amplification of SEQ ID NO: 162.
[0077] SEQ ID NO: 41 is a forward PCR primer for the amplification of SEQ ID NO: 163.
[0078] SEQ ID NO: 42 is a reverse PCR primer for the amplification of SEQ ID NO: 163.
[0079] SEQ ID NO: 43 is a forward PCR primer for the amplification of SEQ ID NO: 164.
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[0081] SEQ ID NO: 45 is a forward PCR primer for the amplification of SEQ ID NO: 165.
[0082] SEQ ID NO: 46 is a reverse PCR primer for the amplification of SEQ ID NO: 165.
[0083] SEQ ID NO: 47 is a forward PCR primer for the amplification of SEQ ID NO: 166.
[0084] SEQ ID NO: 48 is a reverse PCR primer for the amplification of SEQ ID NO: 166.
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[0086] SEQ ID NO: 50 is a reverse PCR primer for the amplification of SEQ ID NO: 167.
[0087] SEQ ID NO: 51 is a forward PCR primer for the amplification of SEQ ID NO: 168.
[0088] SEQ ID NO: 52 is a reverse PCR primer for the amplification of SEQ ID NO: 168.
[0089] SEQ ID NO: 53 is a forward PCR primer for the amplification of SEQ ID NO: 169.
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[0091] SEQ ID NO: 55 is a forward PCR primer for the amplification of SEQ ID NO: 170.
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[0107] SEQ ID NO: 71 is a forward PCR primer for the amplification of SEQ ID NO: 178.
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[0114] SEQ ID NO: 78 is a reverse PCR primer for the amplification of SEQ ID NO: 181.
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[0150] SEQ ID NO: 114 is a reverse PCR primer for the amplification of SEQ ID NO: 199.
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DEFINITIONS

[0392] A "maturity group value" can be any indicative number, symbol, or combination of both that provides an indication of when a plant will mature.
[0393] A "dominant maturity allele" is an allele that, when present either in single copy (heterozygous) or two copies (homozygous), affects the maturity of the plant.
[0394] A "recessive maturity allele" is an allele that, when present in one copy (heterozygous), does not affect the maturity of a plant.
[0395] As used herein, determinate growth habit refers to ceasing of vegetative growth after the main stem terminates in a cluster of mature pods.
[0396] As used herein, indeterminate growth habit refers to the development of leaves and flowers simultaneously throughout a portion of their reproductive period, with one to three pods at the terminal apex.
[0397] As used herein, an allelic combination is the combination of alleles present at more than one characterized location or loci. An example of an allelic combination is allelic combination 10, which is homozygous dominant at maturity genomic region 1; homozygous recessive at maturity genomic region 2; and homozygous dominant at maturity genomic region 3.
[0398] As used herein, "line" refers to a group of individual plants from the similar parentage with similar traits. An "elite line" is any line that has resulted from breeding and selection for superior agronomic performance. Additionally, an elite line is sufficiently homogenous and homozygous to be used for commercial production. Elite lines may be used in the further breeding efforts to develop new elite lines. An elite plant is any plant from an elite line.
[0399] As used herein, "a trait" refers to an observable and/or measurable characteristic of an organism, such as a trait of a plant, for example, tolerance to an herbicide, insect and microbe. A trait can be conventional and transgenic. Non-limiting examples of traits include herbicide tolerance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance, altered oils production, high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistant, increased digestibility, industrial enzymes, pharmaceutical proteins, peptides and small molecules, improved processing traits, improved flavor, nitrogen fixation, hybrid seed production, reduced allergenicity, biopolymers, and biofuels.
[0400] As used herein, "a transgene" refers to a foreign gene that is placed into an organism by the process of plant transformation. In certain aspects, a soybean plant provided by the invention may comprise one or more transgene(s).
[0401] As used herein, "altered" means increased or decreased at maturity. In this aspect, a mature seed as defined by a seed that is harvested in the field for commercial agricultural practices, such as sale for feed. In an aspect, a soybean plants are selected for preferred geographies for expression of at least one phenotypic trait. The phenotypic trait includes altered levels of a substance or a molecule, such as proteins, oils, or gamma linolenic acid. "Altered" can include any relative increase or decrease of function or production of a gene product of interest, in an aspect up to and including complete elimination of function or production of that gene product. When levels of a gene product are compared, such a comparison is preferably carried out between organisms with a similar genetic background. Preferably, a similar genetic background is a background where the organisms being compared share 50% or greater, more preferably 75% or greater, and, even more preferably 90% or greater sequence identity of nuclear genetic material. In another aspect, a similar genetic background is a background where the plants are isogenic except for one or more markers of the present invention.
[0402] As used herein, a "cultivar" is a race or variety of a plant that has been created or selected intentionally and maintained through cultivation.
[0403] As used herein, the term "tissue culture" indicates a composition comprising isolated cells of the same or a different type or a collection of such cells organized into parts of a plant.

DETAILED DESCRIPTION OF THE INVENTION

[0404] Determination of the maturity group value of a soybean plant or seed is important in selecting where a soybean

plant should be grown. An aspect of the present invention provides for a method of establishing where a plant or seed should be grown. A suitable region of a soybean plant or seed can be established. Establishment of a region can include selection of a suitable maturity belt region. Maturity belts range in the United States from 000 in the extreme northern U.S. to VIII in the southern Gulf Coast states. The present invention can also be used to determine other maturity belts including 1× and X. The present invention can further be utilized to determine whether a plant is suitable for one, two, or more maturity belts or regions.

[0405] A suitable geographic region can be selected using a method of the present invention. In addition to maturity belts, other geographic regions that can be selected include maturity group 0 regions, such as and without limitation, Western Maine, North Dakota, Central Montana, Northwestern Oregon; maturity group 1 regions, such as and without limitation, northern Wisconsin, South Dakota; maturity group 2 regions, such as and without limitation, Vermont, Southern Massachusetts, Northern Connecticut, New York, Central Florida, Michigan, Northern Illinois, Southern Wisconsin, Iowa, Nebraska, Colorado, Central California; maturity group 3 regions, such as and without limitation, Western New Hampshire, Pennsylvania, Ohio, Indiana, Southern Illinois, Northern Missouri, Kansas, Southeast Wyoming, Colorado; maturity group 4 regions, such as and without limitation, Maryland, Northern Virginia, Kentucky, Western West Virginia, Central Missouri, Texas, Western Oklahoma; maturity group 5 regions, such as and without limitation, Central Virginia, North Carolina, Central and Western North Carolina, Mississippi, Louisiana, Tennessee; maturity group 6 regions, such as and without limitation, North Carolina, Eastern South Carolina; and maturity group 7 regions, such as and without limitation, Georgia, and Alabama. In another aspect, a seed of the present invention can be sent to a geographic region that is desirable to optimize a trait, such as yield.

[0406] The present invention also provides methods of selecting a suitable geographic region and methods for determining the maturity group of a soybean plant or seed by genotypic analysis. One aspect of the present invention includes a method of establishing where a soybean plant should be grown by obtaining DNA from the soybean plant; and determining if an allele within maturity genomic region 1 is homozygous or heterozygous using marker SEQ ID NO: 151.

[0407] The present invention allows the determination of allelic combinations. Allelic combinations can be any combination of alleles. In one aspect, it can be a combination of 2, 3, 4, 5, 6, 7, or 8 pairs of alleles that occupy a genetic locus. In another aspect, the alleles can be located within 2, 3, 4, 5, 6, 7, or 8 or more maturity genomic regions. Such maturity regions can be selected from maturity genomic region 1, maturity genomic region 2, maturity genomic region 3, maturity genomic region 4, maturity genomic region 5, maturity genomic region 6, maturity genomic region 7, or maturity genomic region 8, etc.

[0408] Alleles at any combination of maturity regions can be determined individually or in combination. One illustrative combination is a combination of more than one pair of alleles at maturity regions 1, 2, and 3. Another illustrative combination is a combination of more than one pair of alleles at maturity regions 1 and 2. "Allelic combinations" is intended to include, without limitation, any of homozygous dominant, homozygous recessive, and heterozygous alternatives at a particular locus.

[0409] Determination of an allele or the combination of alleles at a locus or loci can be carried out by any appropriate methodology. In an aspect, various assays can be used, such as a Taq-Man® assay, Real Time PCR, and nucleic acid sequencing, and simple sequence repeat mapping, to detect the genotype. In an aspect of the present invention, the assay includes a nucleic acid molecule of the present invention. Nucleic acids include deoxynucleic acids (DNA) and ribonucleic acids (RNA) and functionally equivalent analogues thereof.

[0410] Nucleic acids for use in the present invention can be obtained from a plant, such as from a plant part which includes a leaf, vascular tissue, flower, pod, seed, root, stem, or a portion of any.

[0411] In one aspect, nucleic acids are obtained from a plant or plant part using a non-destructive method. In an aspect, the plant part is a seed. In an aspect, the nucleic acids are obtained from a seed in a non-destructive manner, which provides for a seed that is viable. For example, DNA can be obtained from a seed by chipping the seed with a sharp knife at a part furthest away from the 'eye' or by pricking carefully with a needle to puncture the seed. Any method that will obtain DNA for analysis or allow in situ analysis of the DNA can be used provided that the plant or plant part retains the ability to grow. If DNA is taken from a seed and the seed is still viable, the method can be considered non-destructive. Exemplary methods to sample seeds without affecting the germination viability of the seeds are detailed in US Patent Application Publication 20060042527A1, hereby incorporated by reference. In an aspect, seeds are sampled by feeding the seeds individually to a sampling station, removing a sample from the seed in the sampling station, conveying the sample to a compartment in a sample tray and conveying the seed to a corresponding compartment in a seed tray.

[0412] In an aspect, the maturity genomic region associated with plant maturity and plant growth habit of the present invention is introduced or selected within the genus *Glycine*. The genus *Glycine* includes the wild perennial soybeans and have a wide array of genetic diversity. For example, the cultivated soybean (*Glycine max* (L.) Merr.) and its wild annual progenitor (*Glycine soja* (Sieb. and Zucc.)) belong to the subgenus *Soja*, contain 2n=40 chromosomes, are cross-compatible, usually produce vigorous fertile F_1 hybrids, and carry similar genomes. Crosses between cultivated *Glycine* species and wild perennial *Glycine* species have variable success among accessions.

[0413] The present invention further provides that the selected plant is from the group consisting of members of the genus *Glycine*, more specifically from the group consisting of *Glycine arenaria, Glycine argyrea, Glycine canescens, Glycine clandestine, Glycine curvata, Glycine cyrtoloba, Glycine falcate, Glycine latifolia, Glycine latrobeana, Glycine max, Glycine microphylla, Glycine pescadrensis, Glycine pindanica, Glycine rubiginosa, Glycine soja, Glycine* sp., *Glycine stenophita, Glycine tabacina*, and *Glycine tomentella*. In an aspect the plant of the present invention is selected from an elite *Glycine max* line.

[0414] The present invention also provides a soybean plant selected for a desired plant maturity by screening for a maturity marker in the soybean plant or seed, the selection comprising assaying genomic nucleic acids for the presence of a

marker molecule that is genetically linked to a genomic region associated with a plant maturity in the soybean plant, where the genomic region is also located on a linkage group associated with a soybean plant of a preferred plant maturity.

[0415] Methods of the present invention include determining if a locus contains a polymorphism, or is homozygous or heterozygous at a maturity region selected from maturity genomic region 1, maturity genomic region 2, maturity genomic region 3, maturity genomic region 4, maturity genomic region 5, maturity genomic region 6, maturity genomic region 7, and/or maturity genomic region 8 by detecting a polymorphism within a nucleic acid molecule comprising a sequence or fragment thereof selected from the group consisting of SEQ ID NOs: 143-174, or complements thereof. The present invention includes the identification of alleles at eight maturity group regions. These regions are termed maturity genomic regions 1 through 8.

[0416] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 1 can be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 or more genetic markers selected from the group consisting of NS0093385, NS0093976, NS0096829, NS0097798, NS0098982, NS00995929, NS0099746, NS0103749, NS0123747, NS0124601, NS0125408, NS0128378, and NS0135390. SNP marker DNA sequences for region 1 include those presented as SEQ ID NO: 143 through SEQ ID NO: 155 and can be amplified using the primers indicated as SEQ ID NO: 1 through SEQ ID NO: 26 with probes indicated as SEQ ID NO: 214 through SEQ ID NO: 239. In another aspect, a maturity genomic region 1 is a region associated with SEQ ID NOs: 143-149, 154-155. In another aspect, a maturity genomic region 1 is a region associated with SEQ ID NO: 149 or SEQ ID NO: 151 or both. In an aspect, maturity genomic region 1 can span 1 centiMorgan (cM), 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 149 or SEQ ID NO: 151.

[0417] An aspect of the present invention includes a method of determining if a soybean seed will grow into a soybean plant having a maturity group of III-VI by determining a homozygous or heterozygous marker within the soybean seed using a marker with the nucleic acid sequence of SEQ ID NO: 151. In a preferred aspect, the homozygous marker can be recessive or dominant. In another preferred aspect, the maturity of the plant is delayed where the marker is homozygous dominant.

[0418] Another aspect of the present invention includes a method of determining if a soybean seed will grow into a soybean plant having a maturity group between 0.0-III.0 comprising determining if an 11-basepair insertion within the nucleic acid sequence of SEQ ID NO: 149 exists in the soybean seed.

[0419] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 2 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, or 6 or more genetic markers including those selected from the group consisting of NS0118907, NS0122182, NS0126989, NS097952, NS0123506 and NS0095677. SNP marker DNA sequences for region 2 include those presented as SEQ ID NO: 156 through SEQ ID NO: 161 and can be amplified using the primers indicated as SEQ ID NO: 27 through SEQ ID NO: 38 with probes indicated as SEQ ID NO: 240 through SEQ ID NO: 251. In another aspect, a maturity genomic region 2 is a region associated with SEQ ID NO: 158. In another aspect, a maturity genomic region 2 is a region associated with SEQ ID NOs: 156-161. In an aspect, maturity genomic region 2 can span 1 cM, 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 158.

[0420] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 3 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 or more genetic markers including those selected from the group consisting of NS0098853, NS0092561, NS0093197, NS0094891, NS0096225, NS0103853, NS0113929, NS0115535, NS0121511, NS0136544, NS0119569, NS0123708, and NS0114317. SNP marker DNA sequences for region 3 including those presented as SEQ ID NO: 162 through SEQ ID NO: 174 and can be amplified using the primers indicated as SEQ ID NO: 39 through SEQ ID NO: 64 with probes indicated as SEQ ID NO: 252 through SEQ ID NO: 277. In another aspect, a maturity genomic region 3 is a region associated with SEQ ID NOs: 164, 167, 171-174. In another aspect, a maturity genomic region 3 is a region associated with SEQ ID NO: 169. In an aspect, maturity genomic region 3 can span 1 cM, 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 169.

[0421] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 4 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, or 6 or more genetic markers including those selected from the group consisting of NS0092743, NS0098176, NS0100078, NS0137415, NS0095530, and NS0129004. SNP marker DNA sequences for region 4 are presented as SEQ ID NO: 175 through SEQ ID NO: 180 and can be amplified using the primers indicated as SEQ ID NO: 65 through SEQ ID NO: 76 with probes indicated as SEQ ID NO: 278-289. In another aspect, a maturity genomic region 4 is a region associated with SEQ ID NO: 178. In an aspect, maturity genomic region 4 can span 1 cM, 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 178. An aspect of the present invention includes a method of detecting maturity genomic region 4 by detecting an allele using a marker selected from any of SEQ ID NO: 175-180.

[0422] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 5 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, or 9 or more genetic markers including those selected from the group consisting of NS0120015, NS0113878, NS0101863, NS0115066, NS0123168, NS0119165, NS0123724, NS0103446, and NS0099024. SNP marker DNA sequences for region 5 including those presented as SEQ ID NO: 181 through SEQ ID NO: 189 and can be amplified using the primers indicated as SEQ ID NO: 77 through SEQ ID NO: 94 with probes indicated as SEQ ID NO: 290 through SEQ ID NO: 307. In another aspect, a maturity genomic region 5 is a region associated with SEQ ID NO: 187. In an aspect, maturity genomic region 5 can span 1 cM, 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 187. An aspect of the present invention includes a method of detecting maturity genomic region 5 by detecting an allele using a marker selected from any of SEQ ID NO: 181-189.

[0423] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 6 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, or 7 or more genetic markers including those selected from the group consisting of NS0116125, NS0125770, NS0103755, NS0125713, NS0124590, NS0119281, and NS0102717.

SNP marker DNA sequences for region 6 including those presented as SEQ ID NO: 190 through SEQ ID NO: 196 and can be amplified using the primers indicated as SEQ ID NO: 95 through SEQ ID NO: 108 with probes indicated as SEQ ID NO: 308 through SEQ ID NO: 321. In another aspect, a maturity genomic region 6 is a region associated with SEQ ID NO: 192. In an aspect, maturity genomic region 6 can span 1 cM, 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 192. An aspect of the present invention includes a method of detecting maturity genomic region 6 by detecting an allele using a marker selected from any of SEQ ID NO: 190-196.

[0424] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 7 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, or 7 or more genetic markers including those selected from the group consisting of NS0095211, NS0099531, NS0099417, NS0097307, NS0103004, NS0102630, and NS0102915. SNP DNA sequences for region 7 including those presented as SEQ ID NO: 197 through SEQ ID NO: 203 and can be amplified using the primers indicated as SEQ ID NO: 109 through SEQ ID NO: 122 with probes indicated as SEQ ID NO: 322 through SEQ ID NO: 335. In another aspect, a maturity genomic region 7 is a region associated with SEQ ID NO: 202. In an aspect, maturity genomic region 7 can span 1 cM, 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 202. An aspect of the present invention includes a method of detecting maturity genomic region 7 by detecting an allele using a marker selected from any of SEQ ID NO: 197-203.

[0425] The state of homozygosity or heterozygosity and dominance or recessivity of maturity genomic region 8 may be monitored by assaying for an allele of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more genetic markers including those selected from the group consisting of N0102362, NS0100652, NS017716, NS0119574, NS0127728, NS0099639, NS0103255, NS0119106, NS0101020, and NS0101779. SNP DNA sequences for region 8 including those presented as SEQ ID NO: 204 through SEQ ID NO: 213 and can be amplified using the primers indicated as SEQ ID NO: 123 through SEQ ID NO: 142 with probes indicated as SEQ ID NO: 336 through SEQ ID NO: 355. In another aspect, a maturity genomic region 8 is a region associated with SEQ ID NO: 204. In an aspect, maturity genomic region 8 can span 1 cM, 5 cM, 10 cM, 15 cM, 20 cM, or 30 cM either side of SEQ ID NO: 204. An aspect of the present invention includes a method of detecting maturity genomic region 8 by detecting an allele using a marker selected from any of SEQ ID NO: 204-213.

[0426] Nucleic acid molecules of the present invention or fragments thereof are capable of specifically hybridizing to other nucleic acid molecules, also included in the present invention, under certain circumstances. In an aspect, the nucleic acid molecules of the present invention contain any of SEQ ID NO: 143-213, complements thereof and fragments of any. In another aspect, the nucleic acid molecules of the present invention include nucleic acid molecules that hybridize, for example, under high or low stringency, substantially homologous sequences, or that have both to these molecules. As used herein, two nucleic acid molecules are capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook et al., In: *Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Press*, Cold Spring Harbor, N.Y. (1989)), and by Haymes et al., In: *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, D.C. (1985). Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. In order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

[0427] As used herein, a substantially homologous sequence is a nucleic acid sequence that will specifically hybridize to the complement of the nucleic acid sequence to which it is being compared under high stringency conditions. The nucleic-acid probes and primers of the present invention can hybridize under stringent conditions to a target DNA sequence. The term "stringent hybridization conditions" is defined as conditions under which a probe or primer hybridizes specifically with a target sequence(s) and not with non-target sequences, as can be determined empirically. The term "stringent conditions" is functionally defined with regard to the hybridization of a nucleic-acid probe to a target nucleic acid (i.e., to a particular nucleic-acid sequence of interest) by the specific hybridization procedure discussed in Sambrook et al., 1989, at 9.52-9.55. See also, Sambrook et al., 1989 at 9.47-9.52, 9.56-9.58; Kanehisa, *Nucl. Acids Res.* 12:203-213, 1984; and Wetmur and Davidson, *J. Mol. Biol.* 31:349-370, 1968. Appropriate stringency conditions that promote DNA hybridization are, for example, 6.0× sodium chloride/sodium citrate (SSC) at about 45° C., followed by a wash of 2.0×SSC at 50° C., are known to those skilled in the art or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y., 1989, 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0×SSC at 50° C. to a high stringency of about 0.2×SSC at 50° C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22° C., to high stringency conditions at about 65° C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

[0428] For example, hybridization using DNA or RNA probes or primers can be performed at 65° C. in 6×SSC, 0.5% SDS, 5×Denhardt's, 100 μg/mL nonspecific DNA (e.g., sonicated salmon sperm DNA) with washing at 0.5×SSC, 0.5% SDS at 65° C., for high stringency.

[0429] It is contemplated that lower stringency hybridization conditions such as lower hybridization and/or washing temperatures can be used to identify related sequences having a lower degree of sequence similarity if specificity of binding of the probe or primer to target sequence(s) is preserved.

Accordingly, the nucleotide sequences of the present invention can be used for their ability to selectively form duplex molecules with complementary stretches of DNA, RNA, or cDNA fragments. Detection of DNA segments via hybridization is well-known to those of skill in the art, and thus depending on the application envisioned, one will desire to employ varying hybridization conditions to achieve varying degrees of selectivity of probe towards target sequence and the method of choice will depend on the desired results.

[0430] As used herein, an agent, be it a naturally occurring molecule or otherwise may be "substantially purified", if desired, referring to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

[0431] The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

[0432] The agents of the present invention may also be recombinant. As used herein, the term recombinant means any agent (e.g. DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

[0433] The agents of the present invention may be labeled with reagents that facilitate detection of the agent (e.g. fluorescent labels (Prober et al., *Science* 238:336-340 (1987); European Patent No. 144914), chemical labels (U.S. Pat. No. 4,582,789; U.S. Pat. No. 4,563,417), modified bases (European Patent No. 119448), all of which are herein incorporated by reference in their entirety).

[0434] In an aspect, an agent of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complements thereof or fragments of either under moderately stringent conditions, for example at about 2.0× SSC and about 65° C. In an aspect, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complements or fragments of either under high stringency conditions.

[0435] Agents of the present invention include genetic markers. Examples of such markers include nucleic acid molecules comprising nucleic acid sequences selected from the group consisting of SEQ ID NOs: 143-213. Examples of public marker databases include, for example: Soybase, an Agricultural Research Service, and United States Department of Agriculture. Other genetic markers are disclosed within.

[0436] Agents of the present invention include fragment nucleic acid molecules of the present invention. Fragments can contain significant portions of, or indeed most of, SEQ ID NOs: 143-213. In an aspect, the fragments are between 100 and 200 consecutive residues, 150 and 300 consecutive residues, 50 and 150 consecutive residues, or 20 and 50 consecutive residues long of a nucleic molecule of the present invention. In another aspect, the fragment comprises at least 50, 100, 200, 300, 400, or 500 consecutive residues of SEQ ID NOs: 143-213. In an aspect, a fragment nucleic acid molecule is capable of selectively hybridizing to SEQ ID NOs: 143-213.

[0437] In one aspect of the present invention, a preferred marker nucleic acid molecule of the present invention has the nucleic acid sequence set forth in SEQ ID NO: 143 through. SEQ ID NO: 213 or complements thereof or fragments of either. In another aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 80% and 100% or 90% and 100% sequence identity with the nucleic acid sequence set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complement thereof or fragments of either. In a further aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 95% and 100% sequence identity with the sequence set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complement thereof or fragments of either. In an aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 98% and 100% sequence identity with the nucleic acid sequence set forth in SEQ ID NO: 143 through SEQ ID NO: 213 or complement thereof or fragments of either.

[0438] The percent identity is preferably determined using the "Best Fit" or "Gap" program of the Sequence Analysis Software Package™ (Version 10; Genetics Computer Group, Inc., University of Wisconsin Biotechnology Center, Madison, Wis.). "Gap" utilizes the algorithm of Needleman and Wunsch to find the alignment of two sequences that maximizes the number of matches and minimizes the number of gaps. "BestFit" performs an optimal alignment of the best segment of similarity between two sequences and inserts gaps to maximize the number of matches using the local homology algorithm of Smith and Waterman. The percent identity calculations may also be performed using the Megalign program of the LASERGENE bioinformatics computing suite (default parameters, DNASTAR Inc., Madison, Wis.). The percent identity is most preferably determined using the "Best Fit" program using default parameters.

[0439] The present invention further provides one or more single nucleotide polymorphism (SNP) markers. The detection of polymorphic sites in a sample of DNA, RNA, or cDNA may be facilitated through the use of nucleic acid amplification methods. Such methods include those that specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

[0440] A method of achieving such amplification employs the polymerase chain reaction (PCR) (Mullis et al. 1986 Cold Spring Harbor Symp. Quant. Biol. 51:263-273; European Patent No. 50,424; European Patent No. 84,796; European Patent No. 258,017; European Patent No. 237,362; European Patent No. 201,184; U.S. Pat. No. 4,683,202; U.S. Pat. No. 4,582,788; and U.S. Pat. No. 4,683,194), using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

[0441] Alleles that associate with plant maturity can be determined based on linkage analysis of plants and nucleic acid molecules of the present invention. A number of molecular genetic maps of *Glycine* have been reported (Mansur et al., *Crop Sci.* 36: 1327-1336 (1996); Shoemaker et al., *Genetics*

144: 329-338 (1996); Shoemaker et al., *Crop Science* 32: 1091-1098 (1992), Shoemaker et al., *Crop Science* 35: 436-446 (1995); Tinley and Rafalski, *J. Cell Biochem. Suppl.* 14E: 291 (1990); Cregan et al., *Crop Science* 39:1464-1490 (1999)). *Glycine max, Glycine soja* and *Glycine max* x. *Glycine soja* share linkage groups (Shoemaker et al., *Genetics* 144: 329-338 (1996)). A linkage group (LG) is a set of genes that tend to be inherited together from generation to generation. As used herein, reference to the linkage groups (LG), D1b; C2; O; L; and I and of *Glycine max* refers to the linkage group that corresponds to linkage groups, D1b, C2, O, L; and I from the genetic map of *Glycine max* (Mansur et al., *Crop Science.* 36: 1327-1336 (1996)); Cregan et al., *Crop Science* 39:1464-1490 (1999), and Soybase, Agricultural Research Service, United States Department of Agriculture.

[0442] Genome-wide surveys revealed SNP markers associated with maturity genomic region 1 are located on linkage group (LG) C2, maturity genomic region 2 is located on LG 0, maturity genomic region 3 is located on LG L, maturity genomic region 4 is located on LG I, maturity genomic region 5 is located on LG L, maturity genomic region 6 is located on LG D1b+W, maturity genomic region 7 is located on LG G, and maturity genomic region 8 is located on LG M.

[0443] In an aspect, the present invention can be used to identify additional markers associated with maturity genomic regions 1-8. The present invention includes a maturity marker within 1 cM, 5 cM, 10 cM, 15 cM, or 30 cM of SEQ ID NO: 143-213. Similarly, one or more markers mapped within 1, 5, 10, 20 and 30 cM or less from the marker molecules of the present invention can be used for the selection or introgression of the region associated with maturity and/or plant growth habit. The present invention includes a maturity marker that is linked with SEQ ID NO: 143-213 and delays maturity. The present invention includes a substantially purified nucleic acid molecule comprising a maturity marker within 5 kilobases, 10 kilobases, 20 kilobases, 30 kilobases, 100 kilobases, 500 kilobases, 1,000 kilobases, 10,000 kilobases, 25,000 kilobases, or 50,000 kilobases of a marker selected from the group consisting of SEQ ID NO: 143-213. The present invention includes a maturity marker within 5 kilobases, 10 kilobases, 20 kilobases, 30 kilobases, 100 kilobases, 500 kilobases, 1,000 kilobases, 10,000 kilobases, 25,000 kilobases, or 50,000 kilobases of any of SEQ ID NO: 143-213 that cosegregates with any of SEQ ID NO: 143-213. Similarly, one or more markers mapped within 5 kilobases, 10 kilobases, 20 kilobases, 30 kilobases, 100 kilobases, 500 kilobases, 1,000 kilobases, 10,000 kilobases, 25,000 kilobases, or 50,000 kilobases or less from the marker molecules of the present invention can be used for the selection or introgression of the region associated with maturity and/or plant growth habit.

[0444] A maturity genomic region is a physical region of a plant chromosome that has been associated with determining a plant's maturity date. A plant is considered mature when 95% of its pods have reached their mature color. In one aspect of the present invention, the maturity date of a plant is the number of days after August 31st in the northern hemisphere. Alleles of maturity genomic regions 1-8 can influence the maturity date of a plant.

[0445] In one aspect, the maturity date of a plant can determine the maturity group of a plant. Herein, relative maturity refers to a soybean plant maturity group subdividing a maturity group into tenths, for example III.5. Relative maturity provides a more exact description of plant maturity. The number following the decimal point refers to the relative earliness or lateness with a maturity group, for example, IV.2 is an early group IV variety and IV.9 is a late group IV.

[0446] In another aspect, maturity group can be determined by reference to a commercialized strain for a maturity group. For example, a commercialized strain with a known maturity group is grown in an experiment with a new soybean line and the relative maturity of the new soybean line is ascertained by counting the number of days after August 31st and comparing to the commercialized strain. Maturity group refers to an industry division of groups of varieties based on a range in latitudes which the plant is best adapted and most productive. Soybean varieties are classified into 13 recognized maturity groups with the designations ranging from maturity groups 000, 00, 0, and I through X, where 000 represents the earliest maturing variety and X represents the latest maturing variety. The maturity groups have corresponding maturity belts.

[0447] Soybean plants in maturity groups 000 to IV have an indeterminate plant habit, while soybean plants in maturity groups V through X have a determinate plant habit. Early maturity varieties (000 to III) are adapted to northern latitudes with longer day lengths with the maturity designation increasing in southern latitudes with shorter day lengths.

[0448] An increase in maturity can correlate with an increase in yield or other traits such as oil concentration. The correlation of plant maturity and other traits confounds the evaluation of potential markers and candidate genes associated with other traits such as yield. Identification of genomic regions associated with plant maturity, but not with another trait, can allow breeders to genetically fix plant maturity within a soybean plant and separately elucidate other traits, such as those associated with yield.

[0449] The present invention includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1, 2, and 3; and assigning a maturity group value to the soybean plant or soybean seed. In a preferred aspect, determining if alleles at a locus are homozygous or heterozygous includes detecting a polymorphism with a nucleic acid molecule having a sequence of any of SEQ ID NOs: 143-174, or complements thereof.

[0450] In another aspect, the present invention includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous; determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1, 2, 3 and 4; and assigning a maturity group value to the soybean plant or soybean seed.

[0451] The present invention also includes a method of providing information about the maturity of a soybean plant or soybean seed by obtaining DNA from the soybean seed or soybean plant and determining the allelic profile at a locus of genomic region 4.

[0452] The present invention also includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed by obtaining DNA from a soybean plant or soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and determining the allelic combination of the alleles within maturity genomic regions 1, 2, and 3.

[0453] In a preferred aspect, the soybean plant or soybean seed is homozygous for the alleles within maturity genomics regions 1, 2, and 3. In a preferred aspect, the homozygous alleles are either dominant or recessive. In another aspect, the soybean plant or soybean seed is homozygous for the alleles within maturity genomics regions 1 and 2. In a preferred aspect, the homozygous alleles are either dominant or recessive. In another aspect, the soybean plant or soybean seed is homozygous for the alleles within maturity genomics regions 2 and 3. In a preferred aspect, the homozygous alleles are either dominant or recessive. In another aspect, the soybean plant or soybean seed is heterozygous for the alleles within maturity genomics regions 1, 2, and 3. In another aspect, the soybean plant or soybean seed is heterozygous for the alleles within maturity genomics regions 1 and 2. In another aspect, the soybean plant or soybean seed is heterozygous for the alleles within maturity genomics regions 2 and 3. In a preferred aspect, the allelic combination is allelic combination 10, allelic combination 11, allelic combination 12, allelic combination 13, allelic combination 14, allelic combination 15, allelic combination 16, allelic combination 17, allelic combination 18, and allelic combination 19.

[0454] An aspect of the present invention includes a method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant by obtaining DNA from a soybean plant or soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining the allelic combination of the alleles within maturity genomic regions 1 and 2; and assigning a maturity growth value to the soybean plant or soybean seed. In a preferred aspect, determining whether an allele is homozygous or heterozygous includes detecting a polymorphism from any of SEQ ID NOs: 143-161. In a preferred aspect, the allelic combination is allelic combination 1, allelic combination 2, allelic combination 3, allelic combination 4, allelic combination 5, allelic combination 6, allelic combination 7, allelic combination 8, and allelic combination 9. In a preferred aspect, the soybean plant or soybean seed is obtained from a cross of an early maturity group parent soybean plant and a mid-maturity parent soybean plant. In a preferred aspect, the early maturity group parent soybean plant is between 00.0-I.0 and the mid-maturity parent soybean plant is between III.0-IV.9

[0455] An aspect of the present invention includes a method to determine if a soybean plant has a maturity group of 0.0-III.9 by determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; and assigning a maturity group value for the soybean plant between 0.0-III.9. In a preferred aspect, maturity in the soybean plant is reached at least 5 days before a soybean plant that is homozygous dominant within maturity genomic region 1, homozygous dominant within maturity genomic region 2 and is grown under the same environmental conditions.

[0456] Another aspect of the present invention includes a method to determine if the maturity of a soybean plant is in a 00.0-III.0 maturity group by determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; and assigning a maturity group value for the soybean plant between 00.0-III.0. In a preferred aspect, a selected soybean seed is homozygous recessive at maturity genomic region 1 and homozygous recessive at maturity genomic region 2 and has a maturity group between 0.5-II.0. In a preferred aspect, a soybean seed is selected that is homozygous recessive at maturity genomic region 1 and heterozygous dominant at maturity genomic region 2 and has a maturity group between 1.5-II.9.

[0457] The present invention includes a method where the maturity group of a progeny plant is predicted by whether an allele in maturity genomic region 1 is homozygous dominant, homozygous recessive, or heterozygous and whether an allele in maturity genomic region 2 is homozygous dominant, homozygous recessive, or heterozygous. In an aspect, if the maturity group of a plant is between 0 and II, the maturity group can be identified by determining the allelic combination of maturity genomic regions 1 and 2 in a plant or seed. See, for example, Table 9.

[0458] In an alternate aspect, if the maturity group of a plant is between III and V, the maturity group can be identified by determining the allelic combination of maturity genomic regions 1, 2 and 3 in a plant or seed. See, for example, Table 9. In an aspect, if the maturity group of a plant is between IV and V, the maturity group can be identified by determining the allelic combination of maturity genomic regions 1, 2 and 3 in a plant or seed. See, for example, Table 9.

[0459] In another aspect, the maturity group of the parent plants is known. In an aspect, the maturity groups of the parent plants are different by more than 10 days, between 10 days—20 days, between 10 days-30 days, more than 2 maturity groups, less than 2 maturity groups, between maturity groups 000 and VI. In an aspect, the maturity group of a progeny plant resulting from a cross with at least one parent having a maturity group of 0-II is identified by determining the allelic combination of maturity genomic regions 1 and 2. In another aspect, the maturity group of a progeny plant resulting from a cross with parent plants having a maturity group of III, IV, V, or III-V is identified by determining the allelic combination of maturity genomic regions 1, 2 and 3.

[0460] In an aspect, more dominant alleles at a locus in a maturity group region correlate with a delay in maturity. In another aspect, an increase in the number of dominant alleles correlates with a delay in maturity.

[0461] In an aspect, parent plants with a difference in maturity group greater than 1.5, 2, 2.5, 3, 3.5 are crossed and their maturity group identified by determining the allelic combination. In an aspect, parent plants with a difference in maturity group between 1 and 3, between 1 and 4, between 2 and 3, between 2 and 5, between 2 and 6, between 2 and 7 are

crossed and their maturity group identified by determining the allelic combination of the progeny. In an aspect, parent plants with a difference in maturity group greater than 1.5, 2, 2.5, 3, 3.5 are crossed and their maturity group identified by determining the allelic combination.

[0462] In an aspect, a progeny plant has a maturity group earlier than one parent by 5, 10, or 15 days. In another aspect a progeny plant has a maturity group later than one parent plant by 5, 10, or 15 days. In an aspect, a progeny plant has a maturity group earlier than both parents by 5, 10, or 15 days. In another aspect, a progeny plant has a maturity group later than both parent plants by 5, 10, or 15 days.

[0463] In an aspect, an early parent of maturity group 0.1 is crossed with a later maturity parent plant that is a 1.9, and the progeny plants with allelic combination 1 are 0.1-0.5 maturity. In another aspect, an early parent with maturity of 0.9 is crossed with a plant having 3.5 maturity, and the plants having allelic combination 1 are maturity group 1.0-1.5.

[0464] In an aspect, the maturity group of a progeny seed is determined from a cross between a very early maturity parent plant with a later maturity parent plant. In an aspect, the very early maturity parent plant is a maturity group 00.0-0.9 and the later maturity parent plant is a maturity group 111.5-IV.5. In an aspect, the very early maturity parent plant is a maturity group 00 and the later maturity parent plant is a maturity group III or IV. In an aspect, DNA can be obtained from plants or plant parts such as seeds in the F_1, F_2, F_3, F_4 or later populations. In an aspect, one or more plants or plant parts are genotyped for alleles in genomic regions 1 and 2. In an aspect, the alleles are determined using the SNP markers NS0128378 (genomic maturity region 1) and NS0118907 (genomic maturity region 2).

[0465] In an aspect, the plants are phenotyped for maturity by counting the number of days after August 31st until a plant matures. In an aspect, a plant is considered mature when 95% of the pods are brown. In an aspect, when alleles from markers associated with maturity genomic regions 1 and 2 are homozygous recessive, the progeny plant will reach maturity 15, 14, 12, 11, 10, 9, or 8 days sooner than the maturity group if the alleles from markers associated with maturity genomic regions 1 and 2 are homozygous dominant. In an aspect, if an allele from a marker associated with maturity genomic region 1 is homozygous dominant and an allele from a marker associated with maturity genomic region 2 is heterozygous, then the progeny plant will reach maturity between 1 day, 1-2 days, 2-3 days, 2-4 days, or 3-5 days earlier than if the alleles from markers associated with maturity genomic regions 1 and 2 are homozygous dominant.

[0466] In another aspect of the present invention, multiple seeds can be selected or bulked. Multiple seeds may include greater than or equal to 2, 3, 4, 5, 6, 10, 50, 100, 500, 1000, 5,000, 10,000 or more seeds. One or multiple seeds can be distributed to a geographic region suitable for growth of one or multiple plants. In this aspect, seeds selected can be distributed or shipped to an appropriate region.

[0467] The present invention also provides multiple soybean seeds in which greater than 50%, 60%, 70%, 80%, 90%, 95%, or 99% of the seeds will grow into plants where the variation in maturity group is within one maturity group, not more than 2 groups or 20 days after August 31st, not more than 1 group or 10 days after August 31st, not more than 0.9 group or nine days after August 31st, not more than 5 days after August 31st or 0.5 group, or with a maturity group between 0.0-II.0, 000.0-III.9. The multiple soybean seeds can grow into soybean plants having indeterminate soybean plant habit or having determinate soybean plant habit. One aspect of the present invention includes a method to select a soybean seed based on indeterminate or determinate growth habit comprising determining if maturity genomic region 3 is homozygous or heterozygous. In one aspect, 85% of the multiple soybean seeds can reach maturity within 10 days, 5 days, 3 days of each other. In another aspect, 95% of the multiple soybean seeds can reach maturity within 10 days, 5 days, 3 days of each other.

[0468] Another aspect of the present invention includes a method to isolate indeterminate-early maturity soybean seeds by obtaining DNA from the soybean seed using a non-destructive method; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; and determining if an allele within maturity genomic region 2 is homozygous or heterozygous.

[0469] Such multiple seeds may be in a container. The container of soybean seeds can contain any number, weight, or volume of seeds. For example, a container can contain at least, or greater than, about 10, 25, 50, 100, 200, 300, 400, 500, 600, 700, 80, 90, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 5000, 7500, or 10,000 or more seeds. In another aspect, a container can contain about, or greater than about, 1 gram, 5 grams, 10 grams, 15 grams, 20 grams, 25 grams, 50 grams, 100 grams, 250 grams, 500 grams, or 1000 grams of seeds. Alternatively, the container can contain at least, or greater than, about 0 ounces, 1 ounce, 5 ounces, 10 ounces, 1 pound, 2 pounds, 3 pounds, 4 pounds, 5 pounds, 10 pounds, 15 pounds, 20 pounds, 25 pounds, 30 pounds, 40 pounds, 50 pounds, 60 pounds, 70 pounds, 80 pounds, 100 pounds, 200 pounds, 300 pounds, 500 pounds, or 1000 pounds or more seeds.

[0470] Containers of soybean seeds can be any container available in the art. For example, a container can be a box, a bag, a can, a packet, a pouch, a tape roll, a pail, or a tube.

[0471] In another aspect, the seeds contained in the containers of soybean seeds can be treated or untreated soybean seeds. In one aspect, the seeds can be treated to improve germination, for example, by priming the seeds, or by disinfection to protect against seed-born pathogens. In another aspect, seeds can be coated with any available coating to improve, for example, plantability, seed emergence, and protection against seed-born pathogens. Seed coating can be any form of seed coating including, but not limited to, pelleting, film coating, and encrustments.

[0472] One aspect of the present invention includes a method of distributing a soybean plant based on maturity group by obtaining DNA from a soybean plant; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and assigning a maturity growth value to the soybean plant; and shipping the soybean plant to a preferred geographic region.

[0473] A plant of the invention may also comprise a gene that confers resistance to insect, pest, viral or bacterial attack. Such a gene may be a transgene. For example, a gene conferring resistance to a pest, such as soybean cyst nematode was described in U.S. Pat. No. 7,154,021, herein incorporated by reference.

[0474] Transgenes may also be used to alter protein metabolism. For example, U.S. Pat. No. 5,545,545, herein

incorporated by reference, describes lysine-insensitive maize dihydrodipicolinic acid synthase (DHPS), which is substantially resistant to concentrations of L-lysine which otherwise inhibit the activity of native DHPS. Similarly, EP 0640141, herein incorporated by reference, describes sequences encoding lysine-insensitive aspartokinase (AK) capable of causing a higher than normal production of threonine, as well as a subfragment encoding antisense lysine ketoglutarate reductase for increasing lysine.

[0475] In another aspect, a transgene may be employed that alters plant carbohydrate metabolism. For example, fructokinase genes are known for use in metabolic engineering of fructokinase gene expression in transgenic plants and their fruit (see U.S. Pat. No. 6,031,154, herein incorporated by reference). A further example of transgenes that may be used are genes that alter grain yield. For example, U.S. Pat. No. 6,486,383, herein incorporated by reference, describes modification of starch content in plants with subunit proteins of adenosine diphosphoglucose pyrophosphorylase ("ADPG PPase"). In EP0797673, herein incorporated by reference, transgenic plants are discussed in which the introduction and expression of particular DNA molecules results in the formation of easily mobilized phosphate pools outside the vacuole and an enhanced biomass production and/or altered flowering behavior. Still further known are genes for altering plant maturity. U.S. Pat. No. 6,774,284, herein incorporated by reference, describes DNA encoding a plant lipase and methods of use thereof for controlling senescence in plants. U.S. Pat. No. 6,140,085, herein incorporated by reference, discusses FCA genes for altering flowering characteristics, particularly timing of flowering. U.S. Pat. No. 5,637,785, herein incorporated by reference, discusses genetically modified plants having modulated flower development such as having early floral meristem development and comprising a structural gene encoding the LEAFY protein in its genome.

[0476] In another aspect, the present invention provides methods and compositions for the preferred deployment of conventional and transgenic traits related to fatty acid synthesis and oil content. Using present invention, breeders can tailor trait integration to geographies for preferred trait expression, whether the trait is conventional (for example, a mutation) or transgenic. For example, a transgene may be employed that alters plant oil biosynthesis and oil composition. In particular, linoleic acid (LA) (18:2, Δ9, 12) is produced from oleic acid (18:1, Δ9) by a Δ12-desaturase (encoded by FAD2) while alpha linolenic acid (ALA) (18:3, Δ9, 12, 15) is produced from LA by a Δ15-desaturase (encoded by FAD3). Moreover, stearidonic acid (SDA) (18:4, Δ6, 9, 12, 15) and gamma linolenic acid (GLA) (18:3, Δ6, 9, 12) are polyunsaturated fatty acids (PUFAs) produced from LA and ALA by a Δ6-desaturase. Various genes encoding desaturases have been described. For example, U.S. Pat. No. 5,952,544, herein incorporated by reference, describes nucleic acid fragments isolated and cloned from *Brassica napus* that encode fatty acid desaturase enzymes. Expression of the *B. napus* Δ15-desaturase of the '544 patent resulted in accumulation of ALA. U.S. Pat. Publication 20060156435, herein incorporated by reference, describes the expression of fungal Δ15-desaturases to increase omega-3 fatty acid profiles in plants. PCT Publication WO05/021761, herein incorporated by reference, discusses genetically engineered plants which produce both SDA and GLA as a result of expressing a Δ6-desaturase and a Δ15-desaturase. Long chain PUFAs such as EPA and DHA can be produced in plants as disclosed in US Pat. Publication 20040172682, herein incorporated by reference.

[0477] Inhibition of the endogenous soy FAD2 gene through use of transgenes that inhibit the expression of FAD2 has been shown to confer a desirable mid-oleic acid (18:1) phenotype (i.e. soybean seed comprising about 50% and 75% oleic acid by weight). Transgenes and transgenic plants that provide for inhibition of the endogenous FAD2 gene expression and a mid-oleic phenotype are disclosed in U.S. Pat. No. 7,067,722, herein incorporated by reference. In contrast, wild type soybean plants that lack FAD2 inhibiting transgenes typically produce seed with oleic acid compositions of less than 20%. Inhibition of the endogenous FAD3 gene gene through use of transgenes that inhibit the expression of FAD3 has been shown to confer a desirable linolenic acid (18:3) phenotype. A "FATB" or "palmitoyl-ACP thioesterase" gene encodes an enzyme (FATB) capable of catalyzing the hydrolytic cleavage of the carbon-sulfur thioester bond in the panthothene prosthetic group of palmitoyl-ACP as its preferred reaction. Hydrolysis of other fatty acid-ACP thioesters may also be catalyzed by this enzyme. Representative FATB-1 sequences include, without limitation, those set forth in U.S Pat. Publication 20040006792 and U.S. Pat. Nos. 5,955,329; 5,723,761; 5,955,650; and 6,331,664, herein incorporated by reference. When the amount of FATB is decreased in a plant cell, a decreased amount of saturated fatty acids such as palmitate and stearate may be provided. Thus, a decrease in expression of FATB may result in an increased proportion of unsaturated fatty acids such as oleic acid (18:1). The simultaneous suppression of FAD2, FAD3, and FATB expression thereby results in driving the FAS pathway toward an overall increase in mono-unsaturated fatty acids of 18-carbon length, such as oleic acid (C18:1). See U.S. Pat. No. 5,955,650, herein incorporated by reference.

[0478] In an aspect, the present invention provides methods and compositions for the preferred deployment of conventional and transgenic traits related to fatty acid synthesis and oil content. Soybean seed oil levels are highly impacted by environment. Oil concentration increases with decreasing latitude, therefore, soybeans in maturity groups 00-I generally have lower oil levels than later maturing soybeans (Yaklich et al. 2002. *Crop Sci* 42:1504-1515). The decrease in oil concentrations is attributed to lower temperatures and shorter growing season (Piper and Boote 1999 J. Am. Oil Chem. Soc. 76:1233-124). In addition, soybeans cultivated under drought stress tend to produce seeds with decreased protein and increased oil (Specht et al. 2001 Crop Sci 41:493-509). Using present invention, breeders can tailor trait integration to geographies for preferred trait expression, whether the trait is conventional (for example, a mutation) or transgenic.

[0479] Genes for altering plant morphological characteristics are also known and may be used in accordance with the invention. U.S. Pat. No. 6,184,440, herein incorporated by reference, discusses genetically engineered plants which display altered structure or morphology as a result of expressing a cell wall modulation transgene. Examples of cell wall modulation transgenes include a cellulose binding domain, a cellulose binding protein, or a cell wall modifying protein or enzyme such as endoxyloglucan transferase, xyloglucan endo-transglycosylase, an expansin, cellulose synthase, or a novel isolated endo-1,4-β-glucanase.

[0480] Methods for introduction of a transgene, for instance to soybean, are well known in the art and include

biological and physical plant transformation protocols. See, for example, Miki et al. (1990), Clemente et al. (Clemente et al., *Crop Sci.,* 40:797-803, 2000), and U.S. Pat. No. 7,002,058, all herein incorporated by reference. A further aspect of the invention relates to tissue cultures of a soybean variety of the invention. Exemplary types of tissue cultures are protoplasts, calli and plant cells that are intact in plants or parts of plants. Plant parts include, but not limited to, embryos, pollen, flowers, leaves, roots, root tips, anthers, vascular tissue, pod, stem, seed, or a portion thereof, or a cell isolated from the plant. In an aspect, the tissue culture comprises plant parts such as embryos, protoplasts, meristematic cells, pollen, leaves or anthers. In these ways, plants of the present invention or parts thereof be grown in culture and regenerated. Exemplary procedures for preparing tissue cultures of regenerable soybean cells and regenerating soybean plants therefrom, are disclosed in U.S. Pat. No. 4,992,375; U.S. Pat. No. 5,015,580; U.S. Pat. No. 5,024,944, and U.S. Pat. No. 5,416,011, each of the disclosures of which is specifically incorporated herein by reference in its entirety. An important ability of a tissue culture is the capability to regenerate fertile plants. For transformation to be efficient and successful, DNA must be introduced into cells that give rise to plants or germ-line tissue.

[0481] In particular, methods for the regeneration of *Glycine max* plants from various tissue types and methods for the tissue culture of *Glycine max* are known in the art (See, for example, Widholm et al., *In Vitro Selection and Culture-induced Variation in Soybean*, In Soybean: Genetics, Molecular Biology and Biotechnology, Eds. Verma and Shoemaker, CAB International, Wallingford, Oxon, England (1996). Regeneration techniques for plants such as *Glycine max* can use as the starting material a variety of tissue or cell types. With *Glycine max* in particular, regeneration processes have been developed that begin with certain differentiated tissue types such as meristems, Cartha et al., *Can. J. Bot.* 59:1671-1679 (1981), hypocotyl sections, Cameya et al., *Plant Science Letters* 21: 289-294 (1981), and stem node segments, Saka et al., *Plant Science Letters,* 19: 193-201 (1980); Cheng et al., *Plant Science Letters,* 19: 91-99 (1980). Regeneration of whole sexually mature *Glycine max* plants from somatic embryos generated from explants of immature *Glycine max* embryos has been reported (Ranch et al., *In Vitro Cellular & Developmental Biology* 21: 653-658 (1985)). Regeneration of mature *Glycine max* plants from tissue culture by organogenesis and embryogenesis has also been reported (Barwale et al., *Planta* 167: 473-481 (1986); Wright et al., *Plant Cell Reports* 5: 150-154 (1986)).

[0482] Once a transgene is introduced into a variety it may readily be transferred by crossing. By using backcrossing, essentially all of the desired morphological and physiological characteristics of a variety are recovered in addition to the locus transferred into the variety via the backcrossing technique. Backcrossing methods can be used with the present invention to improve or introduce a characteristic into a plant (Poehlman and Sleper, In: *Breeding Field Crops*, Iowa State University Press, Ames, 1995; Fehr, *Principles of Cultivar Development* Vol. 1, pp. 2-3 (1987), herein incorporated by reference).

[0483] The present invention includes a method of soybean plant breeding by crossing at least two different parent soybean plants, where the parent soybean plants differ in plant maturity by over 10 days, 10 days-20 days, 10 days-30 days; obtaining a progeny seed from the cross; genotyping a progeny seed of the cross with a genetic marker; and selecting a soybean seed possessing a genotype for preferred maturity. The present invention also includes a method of soybean plant breeding by assaying a soybean plant for the presence of a marker sequences selected from SEQ ID NO: 143 through SEQ ID NO: 213; and associating the soybean plant with a maturity group. The present invention also includes a method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent soybean plant, where the parent soybean plants differ in soybean plant maturity by over 10 days, 10 days-20 days, 10 days-30 days, by crossing a parent soybean plant comprising a desired trait with a second parent soybean plant; obtaining progeny soybean seed from the cross; screening a progeny soybean seed for the trait; screening a progeny soybean seed for a desired maturity group using a marker selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213 to determine the desired geographical growing region; and selecting a progeny soybean seed containing the desired trait and desired soybean plant maturity.

[0484] In an aspect of the present invention, a method of soybean plant breeding includes crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group. In a preferred aspect, the maturity phenotype of the progeny soybean plant or soybean seed is unknown. In another preferred aspect, the progeny is grown under conditions that are unsuitable for determining maturity of the soybean plant. In another preferred aspect, the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days-20 days, 10 days-30 days. herein a maturity phenotype of at least one of the two different parent soybean plants is unknown. In a preferred aspect, the maturity phenotype of both of the two different parent soybean plants is unknown. In a preferred aspect, the progeny soybean plant is not photoperiod sensitive. In another preferred aspect, at least one parent soybean plant is not photoperiod sensitive. In a preferred aspect, both parent soybean plants are not photoperiod sensitive. In a preferred aspect, the maturity genomic region is characterized by a dominant allele identified in Table 6. In a preferred aspect, the maturity genomic region is characterized by a recessive allele identified in Table 6.

[0485] In an aspect of the present invention, at least one or both parent soybean plant are an elite variety. In an aspect of the present invention, a progeny soybean plant is an exotic soybean plant or one or both parent soybean plants are exotic soybean plants.

[0486] An aspect of the present invention includes a method of selecting a soybean plant for germplasm improvement by determining a maturity group by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group; and incorporating the selected soybean plant into a use selected from the group consisting of using the soybean plant for breeding, advancement of the soybean plant through self-fertilization, trait integration, use of soybean plant or parts thereof for transformation, and use of soybean plants or parts thereof for mutagenesis.

[0487] Another aspect of the present invention includes a method of co-selecting a soybean plant for expression of a non-maturity phenotypic trait and a maturity trait by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; nondestructive genotyping a progeny soybean plant or soybean seed of the cross with a genetic marker characterizing a maturity genomic region; and selecting a soybean plant possessing a genotype for a desired maturity group; and to determine the desired geography for the progeny soybean plant growth, and a method for determining the non-maturity phenotype.

[0488] In a preferred aspect, the method for detecting the non-maturity phenotype is a genotypic or phenotypic method. In a preferred aspect, the non-maturity phenotypic trait is any of herbicide tolerance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance, altered oils production, high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistant, increased digestibility, industrial enzymes, pharmaceutical proteins, peptides and small molecules, improved processing traits, improved flavor, nitrogen fixation, hybrid soybean seed production, reduced allergenicity, biopolymers, and biofuels.

[0489] In another preferred aspect, a phenotypic trait is any of altered protein and oil composition, altered levels of a molecule selected from the group consisting of protein, oil, linolenic acid, stearic acid, palmitic acid, oleic acid, linoleic acid, stearidonic acid, alpha-linolenic acid, gamma linolenic acid, docosahexaenoic acid, eicosapentaenoic acid, docosapentaenoic acid, and combinations thereof.

[0490] In one aspect, plants of the present invention can be used in activities related to germplasm improvement, non-limiting examples of which include using the plant for breeding, advancement of the plant through self-fertilization, trait integration, use of plant or parts thereof for transformation, and use of plants or parts thereof for mutagenesis. Non-limiting examples of breeding decisions include progeny selection, parent selection, and recurrent selection for at least one haplotype. In another aspect, breeding decisions relating to development of plants for commercial release comprise advancing plants for testing, advancing plants for purity, purification of sublines during development, variety development, and hybrid development. In yet other aspects, breeding decisions and germplasm improvement activities comprise transgenic event selection, making breeding crosses, testing and advancing a plant through self-fertilization, using plants or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plants or parts thereof for mutagenesis. The choice of breeding method depends on the mode of plant reproduction, the heritability of the trait(s) being improved, and the type of cultivar used commercially (e.g., F_1 hybrid cultivar, pureline cultivar, etc).

[0491] Descriptions of breeding methods that are commonly used for soybeans can be found in one of several reference books (e.g. Fehr, *Principles of Cultivar Development* Vol. 1, pp. 2-3 (1987)).

[0492] In one aspect the present invention includes a method of soybean plant breeding by assaying a soybean plant for the presence of a marker sequences selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213; and associating the soybean plant with a maturity group.

[0493] In another aspect the present invention includes a method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent soybean plant, wherein the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days-20 days, or 10 days-30 days, by crossing a parent soybean plant comprising a desired trait with a second parent soybean plant; obtaining progeny soybean seed from the cross; screening a progeny soybean seed for the trait; screening a progeny soybean seed for a desired maturity group using a marker selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213 to determine the desired geographical growing region; and selecting a progeny soybean seed containing the desired trait and desired soybean plant maturity. In a preferred aspect, the desired trait is transgenic.

[0494] An aspect of the present invention includes a method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 5 days, over 10 days, 10 days-20 days, or days-30 days; obtaining a progeny soybean seed from the cross; genotyping a progeny soybean seed of the cross with a genetic marker; and selecting a soybean seed possessing a genotype for preferred maturity.

[0495] Another aspect of the present invention includes a method of screening soybean seeds based on soybean plant maturity group by obtaining DNA from a soybean seed; determining if an allele within maturity genomic region 1 is homozygous or heterozygous; determining if an allele within maturity genomic region 2 is homozygous or heterozygous; determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and assigning a maturity growth value to the soybean seed.

[0496] One aspect of the present invention is a method of introgressing an allele into a soybean plant by crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; screening the progeny soybean plant of the cross for the allele; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; and selecting a soybean seed, wherein the soybean seed comprises the allele and a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-213. In a preferred aspect, the selected soybean seed further has a second sequence selected from the group consisting of SEQ ID NOs: 143-213. In another preferred aspect, the allele is selected from any or both of SCN resistance and root rot resistance.

[0497] Another aspect of the present invention includes a method of introducing a desired trait into a soybean plant by crossing at least two different parent soybean plants, wherein at least one parent soybean plant has a desired trait; obtaining a progeny soybean seed from the cross; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; assaying the progeny soybean seed of the cross for evidence of the desired trait; and selecting the soybean seed with the desired trait and a desired maturity group. In a preferred aspect, the desired trait is transgenic.

[0498] A further aspect of the present invention includes a method of introgressing an allele into a soybean plant by

crossing at least two different parent soybean plants; obtaining a progeny soybean plant from the cross; obtaining DNA from a soybean seed of the progeny soybean plant using a non-destructive method; and selecting a soybean seed with the allele and a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-174.

[0499] Another aspect of the present invention includes a method of soybean plant breeding by crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 10 days; obtaining progeny soybean seed from the cross; genotyping the progeny soybean seed of the cross with a genetic marker selected from the group consisting of SEQ ID NOs: 143-213; and selecting a soybean seed with a desired maturity group. A further aspect of the present invention includes a soybean plant comprising within its genome an introgressed haplotype associated with maturity, wherein the introgression is facilitated by at least one of the markers from SEQ ID NO: 143-213 or of the markers 143-162.

[0500] Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless expressly specified.

EXAMPLES

Example 1

Discovery of Molecular Markers Associated with Genomic Regions Affecting Plant Maturity

[0501] Soybean is a short day plant, therefore flowering is initiated by short days due to a decrease in photoperiod (Garner & Allard, *J. Agric. Res.* 18, 553-606 (1920)). Consequently, photoperiod (day length) and temperature response of the soybean plant determines areas of plant adaptation. Due to photoperiod sensitivity, soybean genotypes are grown to narrow zones of latitude to optimize yield. Northern soybean varieties, in contrast to Southern varieties, initiate flowering with longer days. Northern varieties planted south of their adaptation zone exhibit accelerated flowering, limited plant growth and reduced yield. Southern soybean varieties planted north of their adaptation zone will have delayed flowering with a potential for frost damage that may reduce yield. Most soybean variety development crosses are made between parents within 10 maturity days of each other. If the parents differ greatly in maturity, progeny plants segregate widely for maturity. In order for breeders to obtain and select for soybean plants of a desire maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive. Identification of genomic regions associated with plant maturity facilitated crosses between parents outside 10 maturity days of each other without maintain a large number of progeny plants.

[0502] To identify genomic regions associated with plant maturity, 258 soybean lines (129 pairs of differing maturity groups) are genotyped with one thousand, four hundred single nucleotide polymorphism (SNP) markers, distributed across the 20 linkage groups of the soybean genetic linkage map. In addition, 258 soybean lines are phenotyped for yield and plant maturity. Associations between SNP marker genotype and plant maturity phenotype are then evaluated. This was done in multiple environments (Tables 2-3).

TABLE 1

Initial identification of maturity genomic regions via marker assisted breeding

Region	Marker	SEQ ID NO:	Effect (Δ d)	P-value
1	NS0125408	148	−0.05071	0.009068
1	NS0098982	155	1.242281	0.01081
2	NS0123506	156	−0.57638	0.021863
3	NS0093197	164	1.274868	1.92E−09
3	NS0136544	171	1.162352	1.33E−10
3	NS0119569	172	−1.87063	3.79E−15
3	NS0114317	174	1.419675	3.01E−08
5	NS0123168	188	−0.21704	0.025498
6	NS0103755	190	−0.02572	0.011701
7	NS0095211	199	−0.09176	2.99E−07
7	NS0097307	200	−0.09023	6.66E−07
7	NS0102630	202	−0.08407	2.26E−06
7	NS0102915	203	−0.08226	5.19E−06
8	NS0100652	206	1.75824	3.92E−06
8	NS0119574	207	0.446757	0.045212
8	NS0101020	212	0.829784	0.000462

TABLE 2

Estimated effect in days of maturity genomic regions

Region	Marker	SEQ ID NO:	Est. effect on plant maturity (Δ d)	Effect (Δd)	P-value
1	NS0124601	143	4.7	0.309636	0.156883
1	NS0096829	145	4.8	0.444689	0.022932
1	NS0099746	146	4.7	0.315142	0.191492
1	NS0123747	147	4.9	0.714394	0.011568
1	NS0125408	148	4.8	0.538569	0.015846
1	NS0128378	149	4.9	0.757069	0.01699
1	NS0093976	154	5.1	0.989792	0.061019
1	NS0098982	155	5.2	1.242281	0.01081
2	NS0123506	156	4.1	0.911763	0.007307
2	NS0097952	157	5.6	4.069668	5.06E−30
2	NS0118907	158	6.3	5.477999	1.01E−33
2	NS0126989	160	4.6	1.994585	0.000191
2	NS0095677	161	3.8	0.473053	0.10136
3	NS0093197	164	5.2	1.274868	1.92E−09
3	NS0103853	167	6	2.937938	3.78E−09
3	NS0136544	171	6.4	3.765493	3.23E−11
3	NS0119569	172	5.8	2.409513	1.72E−21
3	NS0123708	173	6	2.876505	3.44E−26
3	NS0114317	174	5.9	2.627908	1.69E−22
4	NS0098176	176	4.3	1.068684	6.45E−12
4	NS0100078	177	4	0.479955	0.073839
4	NS0095530	179	4.5	1.364994	2.50E−09
4	NS0129004	180	4.5	1.48424	8.04E−08
5	NS0099024	181	3.4	0.732455	0.112193
5	NS0101863	182	3.3	0.434912	0.078906
5	NS0103446	183	3.1	0.181809	0.058299
5	NS0123168	188	3.2	0.217041	0.025498
6	NS0103755	190	1.2	0.609071	0.140857
6	NS0116125	191	0.9	0.456086	0.152892
6	NS0125713	192	1.1	0.566084	0.036335
6	NS0125770	193	0.8	0.414212	0.009099
6	NS0119281	194	1.6	0.797885	0.038077
6	NS0124590	195	1.4	0.706375	0.000889
6	NS0102717	196	1.5	0.749548	0.000246
7	NS0099531	197	1.3	0.636575	0.000701
7	NS0099417	198	2.4	1.181523	0.015954
7	NS0095211	199	1.7	0.835736	0.099501
7	NS0097307	200	0.2	0.090232	6.66E−07
7	NS0102630	202	2.1	1.029761	0.046938
7	NS0102915	203	2.5	1.231387	4.37E−09

TABLE 2-continued

Estimated effect in days of maturity genomic regions

Region	Marker	SEQ ID NO:	Est. effect on plant maturity (Δ d)	Effect (Δd)	P-value
8	NS0102362	204	4.8	2.23831	1.23E-09
8	NS0117716	205	4.3	1.171503	9.09E-06
8	NS0100652	206	4.6	1.75824	3.92E-06
8	NS0119574	207	4.3	1.195594	4.79E-05
8	NS0127728	208	4.5	1.630904	3.33E-07
8	NS0099639	209	4.2	1.037891	0.015656
8	NS0103255	210	4.2	0.975115	0.001037
8	NS0119106	211	4.3	1.18298	0.023909
8	NS0101020	212	4.1	0.829784	0.000462
8	NS0101779	213	4.2	1.000886	0.000563

[0503] The approximate locations of informative markers indicating a state of dominance or recessivity of genomic regions 1, 2, 3, 4, 5, 6, 7, and 8 are determined based upon a survey of polymorphisms among a panel of 258 soybean lines (Table 3 and 4). One factor in choosing these informative markers is based on which marker has the largest effect or is associated with the largest delay in maturity such that it is indicative of the maturity phenotype. Another factor in choosing these informative markers is based on the lowest P value, such that the marker does not get lost in the event of recombination. The markers with lower P value are more likely to be consistently associated with the maturity phenotype across different soybean populations (different parents, different pedigrees). Markers with strong association and predictive of introgression of the genomic region are listed in Table 5. For NS0128378, the SNP is actually an 11-bp indel, were "D" represents the deletion (**********) and "I" represents the insertion (TTCGAAGATTT).

TABLE 3

Position of SNP markers associated with regions 1, 2, 3, 4, 5, 6, 7 and 8.

Region	LG	Position (cM)	Marker	Polymorphism position on Consensus Sequence	SEQ ID NO:
1	C2	113.7	NS0124601	884	143
1	C2	121.9	NS0103749	96	144
1	C2	121.9	NS0096829	225	145
1	C2	121.9	NS0099746	330	146
1	C2	121.9	NS0123747	56	147
1	C2	121.9	NS0125408	133	148
1	C2	121.9	NS0128378	212	149
1	C2	129.3	NS0135390	108	150
1	C2	123	NS0099529	243	151
1	C2	124.3	NS0097798	325	152
1	C2	129.4	NS0093385	109	153
1	C2	134.7	NS0093976	242	154
1	C2	134.7	NS0098982	383	155
2	O	125.4	NS0123506	126	156
2	O	127.7	NS0097952	420	157
2	O	134.9	NS0118907	450	158
2	O	151.4	NS0122182	104	159
2	O	150.8	NS0126989	251	160
2	O	158.5	NS0095677	202	161
3	L	99.4	NS0098853	82	162
3	L	111.5	NS0092561	190	163

TABLE 3-continued

Position of SNP markers associated with regions 1, 2, 3, 4, 5, 6, 7 and 8.

Region	LG	Position (cM)	Marker	Polymorphism position on Consensus Sequence	SEQ ID NO:
3	L	99.4	NS0093197	225	164
3	L	100.4	NS0094891	83	165
3	L	99.4	NS0096225	471	166
3	L	136.2	NS0103853	341	167
3	L	114.2	NS0113929	685	168
3	L	114.2	NS0115535	433	169
3	L	113.6	NS0121511	512	170
3	L	132.9	NS0136544	208	171
3	L	143.1	NS0119569	262	172
3	L	145.8	NS0123708	530	173
3	L	155.9	NS0114317	331	174
4	I	48.3	NS0092743	217	175
4	I	49.6	NS0098176	92	176
4	I	66.4	NS0100078	1412	177
4	I	58.3	NS0137415	231	178
4	I	33.4	NS0095530	327	179
4	I	32.3	NS0129004	1014	180
5	L	40.1	NS0099024	69	181
5	L	35.7	NS0101863	381	182
5	L	40.1	NS0103446	69	183
5	L	35.9	NS0113878	375	184
5	L	36.8	NS0115066	298	185
5	L	36.9	NS0119165	181	186
5	L	36.8	NS0120015	449	187
5	L	36	NS0123168	75	188
5	L	38.8	NS0123724	42	189
6	D1b + W	172.5	NS0103755	45	190
6	D1b + W	164.1	NS0116125	409	191
6	D1b + W	176.3	NS0125713	392	192
6	D1b + W	165.4	NS0125770	1074	193
6	D1b + W	134.8	NS0119281	596	194
6	D1b + W	157.6	NS0124590	1092	195
6	D1b + W	177.2	NS0102717	402	196
7	G	111.5	NS0099531	287	197
7	G	122.1	NS0099417	408	198
7	G	125.7	NS0095211	251	199
7	G	125.7	NS0097307	426	200
7	G	130.4	NS0103004	430	201
7	G	132.1	NS0102630	186	202
7	G	131.2	NS0102915	193	203
8	M	37.7	NS0102362	74	204
8	M	42.2	NS0117716	74	205
8	M	44.2	NS0100652	247	206
8	M	44.2	NS0119574	367	207
8	M	42.8	NS0127728	650	208
8	M	48.8	NS0099639	362	209
8	M	64.8	NS0103255	289	210
8	M	64.8	NS0119106	417	211
8	M	67.1	NS0101020	238	212
8	M	67.1	NS0101779	147	213

[0504] Allele-specific fluorescence-resonance-energy-transfer (FRET) probes are used in Real-Time PCR assays. Two FRET probes bearing different fluorescent reporter dyes are used, where a unique dye is incorporated into an oligonucleotide that can anneal with high specificity to only one of the two alleles. The reporter dyes are 2'-chloro-7'-phenyl-1, 4-dichloro-6-carboxyfluorescein (VIC) and 6-carboxyfluorescein phosphoramidite (FAM).

TABLE 4

Listing of SNP markers associated with regions 1, 2, 3, 4, 5, 6, 7 and 8.

Region	Marker	SEQ ID NO:	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	SEQ ID NO: FAM Probe	FAM Allele	SEQ ID NO: VIC probe	VIC allele
1	NS0124601	143	1	2	214	T	215	G
1	NS0103749	144	3	4	216	G	217	A
1	NS0096829	145	5	6	218	C	219	A
1	NS0099746	146	7	8	220	G	221	A
1	NS0123747	147	9	10	222	T	223	A
1	NS0125408	148	11	12	224	T	225	C
1	NS0128378	149	13	14	226	TTCGAAGATTT	227	**********
1	NS0135390	150	15	16	228	T	229	G
1	NS0099529	151	17	18	230	T	231	A
1	NS0097798	152	19	20	232	G	233	A
1	NS0093385	153	21	22	234	T	235	C
1	NS0093976	154	23	24	236	G	237	C
1	NS0098982	155	25	26	238	C	239	*
2	NS0123506	156	27	28	240	T	241	G
2	NS0097952	157	29	30	242	G	243	A
2	NS0118907	158	31	32	244	C	245	A
2	NS0122182	159	33	34	246	T	247	C
2	NS0126989	160	35	36	248	T	249	A
2	NS0095677	161	37	38	250	T	251	C
3	NS0098853	162	39	40	252	AG	253	**
3	NS0092561	163	41	42	254	T	255	C
3	NS0093197	164	43	44	256	G	257	A
3	NS0094891	165	45	46	258	T	259	G
3	NS0096225	166	47	48	260	C	261	A
3	NS0103853	167	49	50	262	T	263	C
3	NS0113929	168	51	52	264	G	265	C
3	NS0115535	169	53	54	266	T	267	G
3	NS0121511	170	55	56	268	T	269	C
3	NS0136544	171	57	58	270	T	271	C
3	NS0119569	172	59	60	272	T	273	A
3	NS0123708	173	61	62	274	G	275	A
3	NS0114317	174	63	64	276	G	277	A
4	NS0092743	175	65	66	278	AGAA	279	****
4	NS0098176	176	67	68	280	T	281	C

TABLE 4-continued

Listing of SNP markers associated with regions 1, 2, 3, 4, 5, 6, 7 and 8.

Region	Marker	SEQ ID NO:	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	SEQ ID NO: FAM Probe	FAM Allele	SEQ ID NO: VIC probe	VIC allele
4	NS0100078	177	69	70	282	T	283	G
4	NS0137415	178	71	72	284	T	285	C
4	NS0095530	179	73	74	286	T	287	A
4	NS0129004	180	75	76	288	G	289	A
5	NS0099024	181	77	78	290	G	291	A
5	NS0101863	182	79	80	292	G	293	A
5	NS0103446	183	81	82	294	G	295	A
5	NS0113878	184	83	84	296	G	297	A
5	NS0115066	185	85	86	298	T	299	A
5	NS0119165	186	87	88	300	G	301	A
5	NS0120015	187	89	90	302	G	303	C
5	NS0123168	188	91	92	304	T	305	C
5	NS0123724	189	93	94	306	G	307	A
6	NS0103755	190	95	96	308	T	309	A
6	NS0116125	191	97	98	310	T	311	C
6	NS0125713	192	99	100	312	G	313	A
6	NS0125770	193	101	102	314	G	315	A
6	NS0119281	194	103	104	316	G	317	A
6	NS0124590	195	105	106	318	T	319	C
6	NS0102717	196	107	108	320	G	321	A
7	NS0099531	197	109	110	322	AA	323	**
7	NS0099417	198	111	112	324	G	325	C
7	NS0095211	199	113	114	326	T	327	C
7	NS0097307	200	115	116	328	G	329	C
7	NS0103004	201	117	118	330	G	331	A
7	NS0102630	202	119	120	332	C	333	A
7	NS0102915	203	121	122	334	C	335	A
8	NS0102362	204	123	124	336	T	337	C
8	NS0117716	205	125	126	338	ACTT	339	****
8	NS0100652	206	127	128	340	T	341	A
8	NS0119574	207	129	130	342	G	343	A
8	NS0127728	208	131	132	344	G	345	A
8	NS0099639	209	133	134	346	T	347	C

TABLE 4-continued

Listing of SNP markers associated with regions 1, 2, 3, 4, 5, 6, 7 and 8.

Region	Marker	SEQ ID NO:	SEQ ID NO: Forward Primer	SEQ ID NO: Reverse Primer	SEQ ID NO: FAM Probe	FAM Allele	SEQ ID NO: VIC probe	VIC allele
8	NS0103255	210	135	136	348	T	349	C
8	NS0119106	211	137	138	350	C	351	A
8	NS0101020	212	139	140	352	C	353	C
8	NS0101779	213	141	142	354	G	355	C

TABLE 5

Most predictive markers for genomic regions associated with plant maturity and/or growth habit of soybean plants

Region	Marker	SEQ ID NO:	Rec. Allele	Dom. Allele
1	NS0099529	151	A	T
1	NS0128378	149	**********	TTCGAAGATTT
2	NS0118907	158	A	C
3	NS0115535	169	T	G
4	NS0137415	178	C	T
5	NS0120015	187	C	G
6	NS0125713	192	A	G
7	NS0102630	202	C	A
8	NS0102362	204	C	T

[0505] SNP markers associated with region 1 include SEQ ID NO: 143 through SEQ ID NO: 155. All of these SNP makers for region 1 map to a region on linkage group C2. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 1 through SEQ ID NO: 26, and probes indicated as SEQ ID NO: 214 through SEQ ID NO: 239.

[0506] SNP markers associated with region 2 include SEQ ID NO: 156 through SEQ ID NO: 161. All of these SNP makers for region 2 map to a region on linkage group O. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 27 through SEQ ID NO: 38, and probes indicated as SEQ ID NO: 240 through SEQ ID NO: 251.

[0507] SNP markers associated with region 3 include SEQ ID NO: 162 through SEQ ID NO: 174. All of these SNP makers for region 3 map to a region on linkage group L. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 39 through SEQ ID NO: 64, and probes indicated as SEQ ID NO: 252 through SEQ ID NO: 277.

[0508] SNP markers associated with region 4 include SEQ ID NO: 175 through SEQ ID NO: 180. All of these SNP makers for region 4 map to a region on linkage group I. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 65 through SEQ ID NO: 76 and probes indicated as SEQ ID NO: 278 through SEQ ID NO: 289.

[0509] SNP markers associated with region 5 include SEQ ID NO: 181 through SEQ ID NO: 189. All of these SNP makers for region 5 map to a region on linkage group L. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 77 through SEQ ID NO: 94, and probes indicated as SEQ ID NO: 290 through SEQ ID NO: 307.

[0510] SNP markers associated with region 6 include SEQ ID NO: 190 through SEQ ID NO: 196 of these SNP makers for region 6 map to a region on linkage group D1b. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 95 through SEQ ID NO: 108, and probes indicated as SEQ ID NO: 308 through SEQ ID NO: 321.

[0511] SNP markers associated with region 7 include SEQ ID NO: 197 through SEQ ID NO: 203. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 109 through SEQ ID NO: 122, and probes indicated as SEQ ID NO: 322 through SEQ ID NO: 333.

[0512] SNP markers associated with region 8 include SEQ ID NO: 204 through SEQ ID NO: 213 of these SNP makers map. Table 4 lists sequences for PCR amplification primers, indicated as SEQ ID NO: 123 through SEQ ID NO: 142 and probes indicated as SEQ ID NO: 336 through SEQ ID NO: 355.

Example 2

Identifying Allelic Combinations of Genomic Regions Associated with Plant Maturity in Early Maturity Group Soybeans

[0513] Genomic regions 1 and 2 are used to predict the plant maturity of progeny plant resulting from a cross between early maturity and mid-maturity parents (III-V). In particular, the allelic combinations of genomic regions 1 and 2 are correlated with a delay in plant maturity. To determine the correlation between allelic combinations of region 1 and 2 and delay in plant maturity, three populations are developed from crossing an early maturity parent (maturity group 00) with a mid-maturity parent (maturity group III or IV) (Table

6). Populations 1-3 are used to determine the association of the composition of genomic regions 1 and 2 with delay in plant maturity.

TABLE 6

Maturity group phenotype of parents in soybean populations

Population	Maturity Group of Female Parent	Maturity Group of Female Parent
1	00.9	3.1
2	00.9	3.4
3	00.9	4.1
4	5.9	4.7
5	5.9	5.1
6	5.8	4.7
7	4.1	00.9
8	3.1	00.9
9	3.4	00.9

[0514] The three populations segregate widely for maturity and are polymorphic at genomic regions 1 and 2. F_3 seed are obtained by selecting one pod per F_2 plant (modified single seed descent). The F_3 populations are planted in Guelph, ON and 1,214 F_3 individuals from all three populations are phenotyped for genomic regions 1 and 2 with the SNP markers NS0128378 (genomic region 1) and NS0118907 (genomic region 2). Individual plants in the F_3 populations are also genotyped for maturity by counting the number of days after August 31st until plant matures; plants are considered mature when 95% of the pods were brown. The procedure is repeated with 1055 of the individual plants where each plant row is grown in Chile and phenotyped for maturity by counting the number of days after March 1st until plant matures; plants are considered mature when 95% of the pods are brown. The procedure is repeated with experimental breeding lines developed from 88 of the 1055 individual plants. Table 8 compares the days to maturity of individual plants across all three populations and the genotype of the individuals at genomic regions 1 and 2. The markers associated with 1 and 2 explain 64% of the variation in plant maturity in year 1 and 94% of the variation in plant maturity in year 2.

TABLE 7

The association of days to maturity with composition of regions 1 and 2. Presence (1) or absence (0) of dominant allele indicated. Homozygous allele states are 0, 0 and 1, 1. Heterozygous allele state is 0, 1.

Allelic			Days to Maturity (D after August 31st)	
Combination	Region 1	Region 2	Year 1	Year 2
1	0, 0	0, 0	19.2	9.5
2	0, 0	0, 1	25.7	13.5
3	0, 0	1, 1	33.6	15.5
4	0, 1	0, 0	26.2	16.4
5	0, 1	0, 1	40.3	ND
6	0, 1	1, 1	49.1	19.5
7	1, 1	0, 0	34.2	17.11
8	1, 1	0, 1	49.3	22.7
9	1, 1	1, 1	53.5	23.9
		Correlation:	64%	94%

Example 3

Identifying Allelic Combinations of Genomic Regions Associated with Plant Maturity in Late Maturity Group Soybeans

[0515] Genomic regions 1, 2, and 3 are used to predict the plant maturity of progeny plant resulting from a cross between late maturity and mid-maturity parents. In particular, some of the allelic combinations of genomic regions 1, 2 and 3 are correlated with a delay in plant maturity (Table 8 and 9). To determine the correlation between allelic combinations of region 1, 2 and 3 and delay in plant maturity, three F_3 populations are developed from crossing a late maturity group V with a late maturity group IV. The populations 4-6 following crosses are used to determine the association of the composition of genomic regions 1, 2 and 3 with delay in plant maturity.

[0516] The three segregate widely for maturity and are polymorphic at genomic regions 1, 2, and 3. F_3 seed are obtained by selecting one seed per F_2 plant (single seed descent). 5,984 F_3 individuals from all three population are genotyped with the SNP markers NS0099529 (genomic region 1), NS0118907 (genomic region 2), and NS0115535 (genomic region 3) and seeds with the same marker haplotype are bulked. F_3 seeds are planted.

TABLE 8

Summary of days to flowering for soybean lines containing various compositions of genomic regions 1, 2, and 3 for plant maturity. Presence (1) or absence (0) of dominant allele indicated. Homozygous allele states are 0, 0 and 1, 1. Heterozygous allele state is 0, 1. ND = no data.

Allelic	Region		Region	Days to flowering (DAP)		
Combination	1	Region 2	3	Pop. 4	Pop. 5	Pop. 6
10	1, 1	0, 0	1, 1	57	57	57
11	1, 1	1, 0	1, 1	58	57	58
12	1, 1	1, 1	0, 0	58	59	55
14	1, 1	0, 0	0, 0	ND	ND	54
15	0, 1	0, 1	0, 1	59	57	56
16	0, 0	1, 1	1, 1	43	36	41
17	0, 0	0, 0	1, 1	44	38	45
18	0, 0	1, 1	0, 0	44	39	44
19	0, 0	0, 0	0, 0	44	38	43

[0517] The individuals are also phenotyped for maturity by counting the number of days after August 31st until plant matures; plants are considered mature when 95% of the pods were brown. Genomic region 3 influences the time of maturity (Tables 8 and 9).

TABLE 9

Summary of days to plant maturity for soybean lines containing various compositions of genomic regions 1, 2, and 3 for plant maturity.

Allelic	Days to Maturity (D after Aug		
Combination	Pop. 4	Pop 5	Pop 6
10	59	58	58
11	54	58	58
12	59	57	59
14	ND	ND	58
15	54	54	53
16	41	35	37
17	37	35	38

TABLE 9-continued

Summary of days to plant maturity for soybean lines containing various compositions of genomic regions 1, 2, and 3 for plant maturity.

Allelic	Days to Maturity (D after Aug		
Combination	Pop. 4	Pop 5	Pop 6
18	44	44	43
19	38	42	43

ND = no data.

Example 4

Discovery of Molecular Markers Associated with Genomic Regions Affecting Plant Growth Habit

[0518] Plant growth habit is an important characteristic for late maturity group growing regions. To identify genomic regions associated with plant growth habit, three F_3 populations are developed from crossing a late maturity group V (determinate growth habit) with a late maturity group IV (indeterminate growth habit). Populations 4-6 are used to determine the association of the genomic region 3 with plant habit (Table 6). Seven hundred and seventy-four soybean lines are screened with the markers associated with genomic region 3. The three populations segregated widely for maturity and are polymorphic at genomic region 3. F_3 seed are obtained by selecting one seed per F_2 plant (single seed descent). 5,984 F_3 individuals from all three population were phenotyped with the SNP NS0115535 (genomic region 3) and seeds with the same marker haplotype are bulked. F_3 seeds are planted. A single marker, NS00115535, is determined to be most predictive and able to separate determinant group V varieties from indeterminant group IV and earlier varieties.

Example 5

Genomic Regions Associated with Growth Habit and Maturity Independent of Yield

[0519] Plant maturity and yield are closely associated in soybean. An increase of one day in maturity may be equivalent to a ~0.7 bu/A increase in yield. The correlation of plant maturity and yield confounds the evaluation of potential QTLs and candidate genes associated with yield. Identification of genomic regions associated with plant maturity allows breeders to genetically fix plant maturity within a soybean plant and elucidate traits associated with yield.

[0520] Three soybean populations are generated from crossing a maturity group 0 with a maturity group III or IV. Populations 7-9 are used (Table 5). The progeny seed planted in Chile and then harvested seeds from those progeny plants are selected in Chile and the plants are grown in Ontario in 2006. Eighty-four progeny are screened with markers associated maturity regions 1 and 2 and evaluated for maturity days and yield (Table 10-12). Markers associated with regions 1 and 2 select for maturity and are independent of yield. For example, Progeny 0430 has significantly higher yield than Progeny 0083 (Table 11). The higher yield of Progeny 0430 is not attributed to differences in plant maturity due similar days to maturity and allelic states of maturity genomic regions 1 and 2.

TABLE 10

Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity Days	Allelic combination
Population 8	0117	30.93	5.50	1
Population 8	0140	29.18	6.50	1
Population 8	0234	32.84	6.50	1
Population 8	0043	34.67	6.50	1
Population 8	0267	36.80	7.00	1
Population 8	0276	40.67	7.50	1
Population 8	0243	42.88	9.50	1
Population 8	0198	39.56	10.50	1
Population 8	0325	33.42	11.00	1
Population 8	0011	39.92	11.50	1
Population 8	0390	41.22	11.50	1
Population 8	0418	44.05	11.50	1
Population 8	0119	41.62	9.50	2
Population 8	0069	37.68	10.00	2
Population 8	0274	38.90	10.00	2
Population 8	0165	43.03	10.00	2
Population 8	0219	39.67	12.50	2
Population 8	0373	49.22	13.00	2
Population 8	0089	50.41	17.00	2
Population 8	0186	43.74	18.00	2
Population 8	0395	43.20	9.50	3
Population 8	0426	41.12	10.00	3
Population 8	0256	43.83	10.00	3
Population 8	0216	45.47	10.50	3
Population 8	0367	47.94	11.50	3
Population 8	0266	42.86	14.00	3
Population 8	0285	42.04	16.00	3
Population 8	0277	50.47	16.00	3
Population 8	0188	45.62	17.50	3
Population 8	0143	44.47	13.50	4
Population 8	0101	41.22	14.50	4
Population 8	0366	41.79	16.50	4
Population 8	0340	47.41	11.50	7
Population 8	0359	46.10	14.50	7
Population 8	0184	46.24	14.50	7
Population 8	0158	43.08	16.00	7
Population 8	0401	50.95	16.00	7
Population 8	0255	47.26	17.00	7
Overall Mean		42.78	12.00	
Non-Check Mean		42.60	12.38	
Check Mean		44.08	9.25	
# Locs		3	2	
# Reps		3	2	
CV		9.978	15.094	
LSD(.05)		6.989	3.640	
F-Statistic		4.525	7.670	
P-Value		0.000	0.000	
Repeatability		0.781	0.870	
Root MSE		4.269	1.811	

TABLE 11

Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity (D)	Allelic Combination
Population 9	0381	38.46	11.00	1
Population 9	0473	40.89	12.50	1
Population 9	0371	36.86	9.00	2
Population 9	0380	31.86	10.00	2
Population 9	0263	43.01	11.00	2
Population 9	0396	38.97	12.00	2
Population 8	0083	29.01	15.00	2
Population 8	0430	42.65	15.00	2

TABLE 11-continued

Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity (D)	Allelic Combination
Population 9	0299	39.96	16.00	2
Population 8	0076	42.95	22.00	2
Population 9	0142	32.31	11.50	3
Population 9	0487	27.86	14.00	3
Population 8	0240	43.66	15.50	3
Population 9	0317	46.74	16.50	3
Population 8	0392	38.21	18.50	3
Population 9	0206	45.77	19.00	3
Population 9	0254	44.06	19.50	3
Population 8	0280	48.22	26.50	3
Population 9	0262	41.41	17.50	4
Population 9	0173	43.17	23.50	4
Population 9	0032	33.65	13.50	6
Population 9	0166	40.72	11.50	7
Population 9	0188	42.19	16.50	7
Population 9	0117	47.98	19.00	7
Population 8	0229	45.34	20.00	7
Population 9	0437	43.25	20.50	7
Population 9	0077	34.05	10.50	8
Population 9	0078	47.66	17.00	8
Population 9	0187	37.18	27.00	8
Population 8	0230	47.26	20.50	9
Population 9	0368	46.49	21.50	9
Population 9	0505	34.06	23.50	9
Overall Mean		39.96	15.69	
Non-Check Mean		40.38	16.57	
Check Mean		37.07	9.50	
# Locs		3	2	
# Reps		3	2	
CV		15.453	13.984	
LSD(.05)		10.105	4.434	
F-Statistic		2.546	10.862	
P-Value		0.000	0.000	
Repeatability		0.609	0.908	
Root MSE		6.176	2.194	

TABLE 12

Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity (D)	Allelic Combination
Population 7	0121	35.25	8.50	1
Population 7	0107	30.98	10.50	1
Population 7	0251	36.59	10.50	1
Population 7	0377	34.51	11.00	1
Population 7	0375	34.34	11.50	1
Population 7	0326	30.51	13.00	1
Population 7	0216	42.26	10.50	2
Population 7	0312	36.15	18.00	2
Population 7	0298	41.40	19.00	2
Population 7	0205	39.41	13.00	3
Population 7	0139	38.59	14.50	3
Population 7	0365	38.14	13.00	4
Population 7	0004	39.79	12.50	5
Population 7	0361	47.75	24.00	8
Overall Mean		39.37	12.55	
Non-Check Mean		37.79	13.57	
Check Mean		44.10	9.50	
# Locs		3	2	
# Reps		3	2	
CV		16.518	11.343	
LSD(.05)		10.749	2.979	
F-Statistic		3.074	16.491	

TABLE 12-continued

Summary of yield, maturity and the allelic combination for maturity regions 1 and 2.

Pedigree	Progeny ID No.	Best Est. Yield (Bu/A)	Maturity (D)	Allelic Combination
P-Value		0.002	0.000	
Repeatability		0.675	0.939	
Root MSE		6.503	1.423	

Example 6

Utilization of Molecular Markers Associated with Plant Maturity to Select Geographic Region for Planting Seed

[0521] Soybean genotypes are grown to narrow zones of latitude to optimize yield due to photoperiod sensitivity. Northern soybean varieties, in contrast to Southern varieties, initiate flowering with longer days. Northern varieties planted south of their adaptation zone exhibit accelerated flowering, limited plant growth and reduced yield. Southern soybean varieties planted north of their adaptation zone have delayed flowering with a potential for frost damage that may reduce yield. When the parents differ in plant maturity greater than 10 day, the progeny of the cross segregate widely for plant maturity. Molecular markers associated with plant maturity genomic regions allows breeders to cross with parents that differ in maturity greater than 10 days, select seed of the cross to grow in the appropriate maturity zone.

[0522] A BC_2F_1 soybean population is generated by crossing MG III.5 with MG 000 and the seed is selected for the appropriate maturity zone growing region using the molecular markers associated with plant maturity. Ninety-three BC_2F_1 plants are screened with 106 SNP markers to evaluate the genetic similarity to the recurrent MG III.5 parent (Table 13). Additionally, the SNP markers included markers associated with the maturity genomic regions 1, 2, 3, 4, and 5. Each individual is heterozygous for at least one maturity genomic region. Individual Progeny: 0107 is heterozygous for 1, 2, 3, 4, and 5 and may be used to select for individual varieties adapted to each maturity group zone. Individuals selected to move forward to the next generation based on adaptation to specific maturity group regions using the allelic combination for the genomic maturity regions.

TABLE 13

Summary of heterozygousity for maturity genomic regions with the F2 generation of MG III.5 parent/(MG III.5 parent * 2/MG 000 parent). Individuals within the population are selected for a geographic maturity group region with SNP markers associated maturity genomic regions.

Plant	Similarity to MGIII.5 parent (%)	Heterozygous for genomic maturity region: 1	2	3	4	5
MG III.5 parent	98.7					
MG 000 parent	2.6					
Progeny: 0050	86.2	x			x	x
Progeny: 0107	85.8			x	x	
Progeny: 0050	84.9	x	x			
Progeny: 0093	84.9	x		x		

TABLE 13-continued

Summary of heterozygousity for maturity genomic regions with the F2 generation of MG III.5 parent/(MG III.5 parent * 2/MG 000 parent). Individuals within the population are selected for a geographic maturity group region with SNP markers associated maturity genomic regions.

Plant	Similarity to MGIII.5 parent (%)	Heterozygous for genomic maturity region: 1	2	3	4	5
Progeny: 0050	82.8		x	x	x	x
Progeny: 0096	82.8			x	x	
Progeny: 0107	82.3		x			
Progeny: 0096	81.9	x			x	
Progeny: 0107	81.5	x	x	x	x	x
Progeny: 0066	60.8				x	
Progeny: 0096	84.1	x		x	x	
Progeny: 0093	82.8	x	x			
Progeny: 0050	81.9	x		x	x	
Progeny: 0050	81.9	x		x		
Progeny: 0096	81.0	x		x	x	
Progeny: 0046	80.6		x	x	x	x
Progeny: 0050	80.2	x	x	x		
Progeny: 0107	80.2	x		x	x	
Progeny: 0093	80.2	x			x	
Progeny: 0096	80.2		x			
Progeny: 0093	79.7	x			x	
Progeny: 0063	79.7			x	x	
Progeny: 0093	79.3		x	x		x
Progeny: 0096	78.9	x		x		
Progeny: 0012	78.9	x			x	x
Progeny: 0085	78.4	x		x	x	
Progeny: 0096	78.0	x				
Progeny: 0107	77.6	x		x		
Progeny: 0063	74.6		x	x	x	
Progeny: 0063	74.1	x		x		
Progeny: 0012	61.2	x	x	x		
Progeny: 0036	61.2	x	x	x		
Progeny: 0012	61.2	x	x			
Progeny: 0093	61.2	x		x	x	x
Progeny: 0012	61.2	x		x		x
Progeny: 0050	61.2	x		x		
Progeny: 0036	61.2	x		x		
Progeny: 0063	61.2	x			x	x
Progeny: 0050	61.2	x			x	
Progeny: 0012	61.2	x			x	
Progeny: 0107	61.2	x				
Progeny: 0012	61.2	x				
Progeny: 0012	60.8	x		x	x	
Progeny: 0012	60.8	x		x	x	
Progeny: 0012	60.8	x		x	x	
Progeny: 0050	60.8	x		x		
Progeny: 0012	60.8	x			x	
Progeny: 0036	60.8	x			x	
Progeny: 0012	60.8	x				
Progeny: 0012	60.8	x				
Progeny: 0036	60.8		x	x	x	
Progeny: 0012	60.8			x	x	
Progeny: 0012	60.3	x	x			
Progeny: 0093	59.9	x	x	x	x	
Progeny: 0096	59.9	x		x	x	
Progeny: 0012	59.9	x		x		
Progeny: 0050	59.9		x	x		x
Progeny: 0085	59.9		x	x		x
Progeny: 0050	59.5	x	x			
Progeny: 0096	59.5	x	x		x	
Progeny: 0036	59.5	x	x		x	
Progeny: 0096	59.5	x		x	x	x
Progeny: 0063	59.5	x		x		
Progeny: 0036	59.5	x		x		
Progeny: 0096	59.5		x			x
Progeny: 0093	58.6	x	x		x	
Progeny: 0050	58.6	x				x
Progeny: 0050	58.6	x				

TABLE 13-continued

Summary of heterozygousity for maturity genomic regions with the F2 generation of MG III.5 parent/(MG III.5 parent * 2/MG 000 parent). Individuals within the population are selected for a geographic maturity group region with SNP markers associated maturity genomic regions.

Plant	Similarity to MGIII.5 parent (%)	Heterozygous for genomic maturity region: 1	2	3	4	5
Progeny: 0093	58.6		x	x	x	
Progeny: 0093	58.2	x	x			
Progeny: 0012	58.2	x	x		x	
Progeny: 0012	58.2	x		x	x	x
Progeny: 0050	58.2	x		x	x	
Progeny: 0012	58.2	x		x	x	
Progeny: 0012	58.2	x		x		
Progeny: 0143	58.2	x		x		
Progeny: 0096	58.2	x			x	
Progeny: 0050	58.2	x			x	
Progeny: 0012	57.8	x	x		x	
Progeny: 0050	57.8	x	x		x	
Progeny: 0012	57.8	x		x		
Progeny: 0093	57.8	x			x	
Progeny: 0093	57.8	x				
Progeny: 0012	57.8		x		x	x
Progeny: 0012	57.8			x	x	
Progeny: 0012	57.8			x	x	
Progeny: 0096	57.3	x		x	x	
Progeny: 0050	56.9	x	x		x	
Progeny: 0093	56.9	x		x	x	
Progeny: 0050	56.9	x		x	x	
Progeny: 0050	56.9	x		x		
Progeny: 0050	56.9			x		x
Progeny: 0096	55.6	x	x		x	x

Example 7

Estimating Effect of Genomic Regions Associated with Maturity

[0523] Each allele of each individual maturity genomic region is associated with a value that can either increase or decrease the relative maturity of a given line. The relative maturity of a given line are predicted by using an additive or epistatic model. The example in Table 14 demonstrates predicting relative maturity based on the allelic combination of the maturity genomic regions. The maturity group of a soybean seed is predicted by the composition of maturity genomic region alleles.

TABLE 14

An example of predicting relative maturity based on additive model

Maturity genomic	Δ Days	Direction
1	10	10
2	5	−5
3	3	−3
4	2	2
5	6	6
6	4	4
7	5	−5
	Sum	9
	Constant	3
	Maturity Days	12
	Maturity Group	1.2

Example 8

Utilization of Molecular Markers Associated with Plant Maturity to Facilitate Crosses with Exotic Germplasm

[0524] The genetic base of cultivated soybean is narrow compared to other field crops. Eighty to ninety percent of cultivated soybean gene pool are traced to 12 plant introductions in northern United State and seven plant introductions in southern United States. Due to the narrow genetic base, soybean is more likely to be impacted by disease and insect attacks. Exotic germplasm helps expand the genetic base of soybean. In addition, exotic germplasm possesses such key traits as disease resistance, insect resistance, nematode resistance, and tolerance to environmental stress. At present, many exotic species are inaccessible in part due to limitations with crossing soybean plants from extremely different maturity groups. Traditionally, breeders must produce and maintain large numbers of progeny plants from crosses between exotic and cultivated germplasm, in order for breeders to select for a small number soybean plants of the desired maturity group. It is often cost prohibitive to maintain the large number of plants required.

[0525] Molecular markers associated with plant maturity facilitate the used of exotic germplasm. Breeders create crosses between exotic and cultivated germplasm. The progeny seed is assayed for plant maturity without expending the resources required to plant and grow large numbers of progeny.

Example 9

Utilization of Molecular Markers Associated with Plant Maturity to Facilitate Introgression of a Transgene

[0526] After a transgene is introduced into a variety, it may readily be transferred to other varieties by crossing. Most soybean variety development crosses are made between parents within 10 maturity days of each other. When parents differ in plant maturity greater than 10 days, the progeny of the cross segregate widely for plant maturity. In order for breeders to obtain and select for soybean plants of the desire maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive. If a transgene is present in a maturity group III variety needs to be transferred to maturity group 0, a direct cross between a maturity group III variety and a maturity group 0 variety is not typically performed. Instead, the transgene is transferred through a series of intermediate crosses between varieties close in plant maturity. Molecular markers associated with plant maturity genomic regions allows breeders to cross parents that differ in maturity greater than 10 days, then select seed of the cross based on the presence of the transgene and the plant maturity phenotype.

Example 10

Utilization of Molecular Markers Associated with Plant Maturity to Facilitate Introgression of a Trait

[0527] If a variety possesses a desirable trait, it may readily be transferred to other varieties by crossing. Most soybean variety development crosses are made between parents within 10 maturity days of each other. When the parents differ in plant maturity greater than 10 days, the progeny of the cross segregate widely for plant maturity. In order for breeders to obtain and select for soybean plants of the desire maturity group, they must produce and maintain a large number of progeny plants, the practice of which is cost prohibitive. If a trait is present in a maturity group III variety needs to be transferred to maturity group 0, a direct cross between a maturity group III variety and a maturity group 0 variety is typically not performed. Instead, the trait is transferred through a series of intermediate crosses between varieties close in plant maturity. Molecular markers associated with plant maturity genomic regions allow breeders to cross with parents that differ in maturity by greater than 10 days and to select seed of the cross based on the presence of the trait and the plant maturity phenotype.

Example 11

Utilization of Molecular Markers Associated with Plant Maturity to Select Environments to Optimize Expression of Traits

[0528] Soybeans cultivated in different environments often perform differently. For instance, a soybean variety may produce seeds with a particular fatty acid profile in one environment and a different fatty acid profile in another environment. A number of environmental factors can influence the expression of traits, including soil type, soil conditions, temperature, photoperiod, geography and cultural practices. Variation in performance of genotypes across different environments is often referred to genotype×environment interactions.

[0529] Soybean seed oil levels are highly impacted by environment. Oil concentration increases with decreasing latitude, therefore, soybeans in maturity groups 00-I generally have lower oil levels than later maturing soybeans (FIG. **1**). Molecular markers associated with plant maturity assist breeders in selecting soybean genotypes and produce plants that are better adapted to a maturity group region to produce higher oil.

[0530] Soybean seed fatty acid composition is highly impacted by the latitude of cultivation. The present invention provides molecular markers associated with plant maturity which are useful for assisting plant breeders to select favorable soybean maturity genotypes to optimize the expression of particular traits in specific geographies, such as fatty acid synthesis, wherein the trait is conventional or transgenic. As used herein, conventional traits include those obtained by mutagenesis. For example, the profile of fatty transgenic soybean plants engineered to produce stearidonic acid (SDA) have a positive correlation with latitude for SDA production and have a negative correlation with latitude for oleic acid, stearic acid, palmitic acid and α-linolenic acid production (Table 15). The percent of SDA increases with increasing latitude (FIGS. **2-3**).

TABLE 15

Correlation of longitude and latitude on fatty acids for mature soybean seed

	Latitude			Longitude		
Fatty Acid	R	P value	N	R	P value	N
stearidonic acid	0.6625*	3.12E−10	71	−0.3748	0.001281263	71
γ-linolenic acid	0.1097	0.362504877	71	−0.0798	0.508051934	71

TABLE 15-continued

Correlation of longitude and latitude on fatty acids for mature soybean seed

	Latitude			Longitude		
Fatty Acid	R	P value	N	R	P value	N
oleic acid	−0.4081*	0.000411819	71	0.167	0.16389379	71
linoleic acid	−0.1581	0.187769857	71	0.0837	0.48752276	71
α-linolenic acid	−0.2403*	0.043495686	71	0.1901	0.112261464	71
palmitic acid	−0.7305*	4.82E−13	71	0.4592	5.62E−05	71
stearic acid	−0.258*	0.029810388	71	−0.1498	0.212583113	71

*significant at 0.05 level

[0531] Latitude is closely related with maturity groups and growing regions. Soybeans are classified into 13 maturity groups (000, 00, 0, I-X) according to the range in latitude in which the plants are adapted and most productive. Group 000 are the earliest maturing and cultivated at the higher latitudes and Group X are the latest maturing and cultivated in lower latitudes. Molecular markers associated with plant maturity will assist breeders in selecting soybean genotypes that are adapted to latitudes known to be associated with preferred SDA production in the plants. As a result, the soybean breeders more efficiently produce plants that are better adapted to the environment and produce higher levels of SDA or other similar traits.

[0532] It is within the scope of this invention to utilize the methods and compositions for preferred trait integration for any trait, conventional or transgenic, affected or influenced by latitude. It is contemplated by the inventors that the present invention will be useful for trait integration of one or more phenotypic traits that are influenced by latitude such that the methods and compositions provided herein will facilitate deployment of one or more traits into preferred germplasm based on maturity, wherein the traits can be conventional or transgenic.

[0533] Having illustrated and described the principles of the present invention, it should be apparent to persons skilled in the art that the invention can be modified in arrangement and detail without departing from such principles. We claim all modifications that are within the spirit, scope and concept of the appended claims.

SEQUENCE LISTING

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<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 1

tgggtgaccc cgaagttg 18

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<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 2

ggcagattcg atactctcgt acgt 24

<210> SEQ ID NO 3
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atgggcaaca gttgtcatat gg 22

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tgatgatggc atggaattat tacc 24

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catttcttca acatccgaac caa 23

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ggaggaaggg tatgcaactt ttac 24

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aaaacggtat atttaacatc caaagca 27

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ccttcccgta aactgaatga tca 23

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ctcacttttg cctttgttag agcat 25

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aaaaaatcac atgatacgag aaaagatct 29

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gttcctagcc aacaatgagt ttctc 25

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cttagtgagc tatgtctaac ttcaatgctt 30

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actgtaaaca atttagcaat caatttgtg 29

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tggtctcggc tgtgaattca g 21

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aatattccat ttatatactt gcacttgca 29

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ggagtgttta gagggatgca ttg 23

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gcgcctatgt cacttaagct gat 23

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acagcaaagg gacacaattc aat 23

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ctctccatat tcaatttgtc aaacttg 27

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tttgggttcc caggtttgc 19

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agaatttaca gcttgcaggt atttaattt 29

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gcaatagttt gagaagctct actacaattt 30

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ttcccttgta tattgttttg aaatgc 26

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tgcagaaaaa cagaaaaaac tgaagt 26

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acaagcatgt tggaccagct t 21

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tgcaagggta tgtcatagtg gaatt 25

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tagaccctta attttatgtt aatttgcgt 29

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atcagtaaaa tggagacaaa tgagtaaaaa 30

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cctaatgttg tagagctcca ggaaag 26

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cataacttcc ttttacatac aatttctata cca 33

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ttattacacc acttgttctt tttaaggaaa 30

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tgtggtccgt tcaaaaatta taatga 26

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caagagaaat ccattaagaa attgca 26

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aaattggtct ttgaaggaaa atgaa 25

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tctggcagtt ctatacttct gaaatttaaa 30

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ctcttaaata gcttatgggt gtatgtcaa 29

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aaattttgga cccatttctt tgc 23

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aattatttgc atttgctctt ggc 23

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<400> SEQUENCE: 65

tgtctgctgg ttgaagtaac ttatgg 26

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gctgatagtt tttgcatatt cttcca 26

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cttgcttaca aattcctcca actaaa 26

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gcttaagaac aaccgagagc tttt 24

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<212> TYPE: DNA
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catgaactgt gattacatat tcttttgc 28

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gctgccgaac atgatggtta 20

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cagaagaaag attctatgac tccaaca 27

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actgcataaa ataccgtaat attctcttga 30

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agaatcatgt gattctgatt gtacga 26

<210> SEQ ID NO 74
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ggaaccaaaa tccctataac tgttgt 26

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attttgggag gacaagtgga ctt 23

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<212> TYPE: DNA
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<400> SEQUENCE: 76

gcaagaaata agatatagcc ttgggtat 28

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<211> LENGTH: 23
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<400> SEQUENCE: 77

tggcatcctc ttatcaacaa agc 23

<210> SEQ ID NO 78
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cctatcagtg ttggtggaag ca 22

<210> SEQ ID NO 79
<211> LENGTH: 22
<212> TYPE: DNA
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ggtgagccaa ggaaagaaac ac 22

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<400> SEQUENCE: 80

cgacgatatg aatcagggaa tagg 24

<210> SEQ ID NO 81
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tggcatcctc ttatcaacaa agc 23

<210> SEQ ID NO 82
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cctatcagtg ttggtggaag ca 22

<210> SEQ ID NO 83
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<400> SEQUENCE: 83

gagaaggatg cttttgaaga gctta 25

<210> SEQ ID NO 84
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acctgactcg gtttctcatt caat 24

<210> SEQ ID NO 85
<211> LENGTH: 30
<212> TYPE: DNA
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<400> SEQUENCE: 85

ggtaaacatt gtcttaccat tattgacatt 30

<210> SEQ ID NO 86
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<212> TYPE: DNA
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catcaacttg cattacataa agtctgatta 30

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aaaaggaaga aaagaagaac aaattttg 28

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agcagaatcc tcacttcaaa gtacag 26

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accaagagga gaaaatctgc ttagg 25

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<223> OTHER INFORMATION: Synthetic Primer

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ccaacaaggg tgcagaaatg a 21

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gggttgcctt gatagttgaa tctg 24

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<400> SEQUENCE: 93

cacttcatct tcaggcatat actcca 26

<210> SEQ ID NO 94
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tcttcaaggc tggttggatg a 21

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tgatggtgaa tatgaagggt ctca 24

<210> SEQ ID NO 96
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 96

aatggaactg ggatttctta ctacaaa 27

<210> SEQ ID NO 97
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 97

tggcaaaagc tagagagcat gat 23

<210> SEQ ID NO 98
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 98

aaccctaacc ttttcttctg ctctt 25

<210> SEQ ID NO 99
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

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<400> SEQUENCE: 99

aactgaaaat tttacattcc tgtcaatg 28

<210> SEQ ID NO 100
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 100

ttctaactga tgacttcaca ctagttttct tat 33

<210> SEQ ID NO 101
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 101

ctcatgtcat catcttacac aaagca 26

<210> SEQ ID NO 102
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 102

cttgtggaga ataagaaaaa ggttcttc 28

<210> SEQ ID NO 103
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 103

tctatatcca aagtctttat atggacacct t 31

<210> SEQ ID NO 104
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 104

ttaaaatcat tacacagtca ctccacaa 28

<210> SEQ ID NO 105
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 105

gtcacaaagc aattccaatt ataacact 28

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<210> SEQ ID NO 106
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 106

aaccttggta aggcaaaaat gcta 24

<210> SEQ ID NO 107
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 107

gggtgctgat tttcataaag ttga 24

<210> SEQ ID NO 108
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 108

gccattctaa tttttgtgga caga 24

<210> SEQ ID NO 109
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 109

taacctctcc tcccccaaac tt 22

<210> SEQ ID NO 110
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 110

gggttgtcct agaactcctg aaga 24

<210> SEQ ID NO 111
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 111

tgttcttgta atcatcaacc agcttaa 27

<210> SEQ ID NO 112
<211> LENGTH: 20

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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 112

gccttctccg ttgcatacca 20

<210> SEQ ID NO 113
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 113

tcacatgcat tagggaattg ctt 23

<210> SEQ ID NO 114
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 114

agcattgtcc caactaagat cttgt 25

<210> SEQ ID NO 115
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 115

atgtattcat tttgaatggg ctacaa 26

<210> SEQ ID NO 116
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 116

gttaaaaatt acaacgccac gaataa 26

<210> SEQ ID NO 117
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 117

ttgcaatttt ttatatcttg atttcacat 29

<210> SEQ ID NO 118
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

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<400> SEQUENCE: 118

gcgaagaatc aaaactggtc aaa 23

<210> SEQ ID NO 119
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 119

acaaggacaa ggctatgaga agtaaga 27

<210> SEQ ID NO 120
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 120

ggccatgaat caagccactt 20

<210> SEQ ID NO 121
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 121

gagttagatt tatccggcaa cga 23

<210> SEQ ID NO 122
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 122

cccgaagaga tgtcatgtta acaa 24

<210> SEQ ID NO 123
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 123

gcgaaaaaca aatttccatt gc 22

<210> SEQ ID NO 124
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 124

agtggtgatg gcatggttga 20

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<210> SEQ ID NO 125
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 125

tcactaagat ctggaattcc aaacc 25

<210> SEQ ID NO 126
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 126

tggaggaaga taagttaaca attaatagca 30

<210> SEQ ID NO 127
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 127

cctgaaaaag ccaatcataa tctaca 26

<210> SEQ ID NO 128
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 128

caggtaggga tgcttcagtg ttg 23

<210> SEQ ID NO 129
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 129

tggaaaagga aagatgatat agcaattt 28

<210> SEQ ID NO 130
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 130

aaccaggaca accacatcaa tct 23

<210> SEQ ID NO 131
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 131

tgatcggatt tgactctttt gtcat 25

<210> SEQ ID NO 132
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 132

ttgcagtttt tgagtatacc actacca 27

<210> SEQ ID NO 133
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 133

atggaagtgg atggaagtag tataatga 28

<210> SEQ ID NO 134
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 134

tttccacatt ttccaatagc ttga 24

<210> SEQ ID NO 135
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 135

tggagctcta ccgaaagttt acaaa 25

<210> SEQ ID NO 136
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 136

caagaactac ctcaaagcca atcc 24

<210> SEQ ID NO 137
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

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<400> SEQUENCE: 137

cttttaaatg gacccagttt gttca 25

<210> SEQ ID NO 138
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 138

tgggttgaag tgaaatggtc aga 23

<210> SEQ ID NO 139
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 139

agcaacaatg actatttcaa ccatttt 27

<210> SEQ ID NO 140
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 140

ccacacctcc ccttggttt 19

<210> SEQ ID NO 141
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 141

cagcaaaatg aatgcaattg gt 22

<210> SEQ ID NO 142
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Primer

<400> SEQUENCE: 142

acattgcaag aactggatgg ttt 23

<210> SEQ ID NO 143
<211> LENGTH: 1040
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 143

agaaagagag aagagtgaag agtgttattt ttttgtttga ctctgaaaaa aaattaagat 60

acaacacatg gcatgattgg agccgtttat atgatcctac gcatgaaaat gtttcaacta 120

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cacatccggt tcccgtcaag aatgggagag gatccgtatg cgatgaactg aacttgaatt 180

gattcattta atatagtgag agagaaaaaa gttaaaccaa tcaaaatggt tgattgcttt 240

agttttatat ttccttttta caaattaacc ctattgttaa cagattaatt tggttaatga 300

atattttatt tctttttat tctctttaat ttcaatcaaa caattttatt ttttactttt 360

tttctattct gtctcattta tttttcattt ctcacgatca aacagaggat tagtctaaaa 420

aaatattaaa taatgcttga ttttattgga actaattctt aatttcatga ccggaatatt 480

cacatgaatt aattgaaaaa tgtgtaagat tggttagatt ggattaattt acttgacttt 540

cttaattgtc tttttatgaa tttgactaac ctaattcttt atttattttg cgaagaaaga 600

agtattattg tatccgtgtg tgtatatata aaataaagtc attcaatcgg tcctaaatta 660

cacaagatac atgtcaaata tgcaaatgaa gtaactcttt gatctgaaaa aaaaaaaaaa 720

aaaaaacaat ccagttttcc cttgtgaaaa aagagctcca aatagcttca ggttgaagca 780

aaaataaaaa attgaagaaa aggttgaagc taaacataaa cctcaaaaac tggtgtacgt 840

cattaacatg ggtgaccccg aagttgccac gtactccaag cgtgtgcggt taacaacgta 900

cgagagtatc gaatctgcct ctgctttctt tcaatttcaa cagaacccat cacacacaca 960

cagaccccat caaccaaaaa caaagaacaa tgattctgag atttgcagca gctgcaggtc 1020

gactctagga aagacccggg 1040

<210> SEQ ID NO 144
<211> LENGTH: 821
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1)..(821)
<223> OTHER INFORMATION: unsure at all n locations; n = a, t, c, or g

<400> SEQUENCE: 144

attccataac ggtttgcaac tcttgaagat cgtgactctg gtcgtgtcac tcctgcgtat 60

cgcgcctggg agcaacaaga ttagttgttc ctctcatggc ttcaatccac cgtttctgct 120

cccattcttc gaaatttcat cggctgcact agtttgtggc ttctctagga caaaatccac 180

aactattttc atgctcatac aaatgcaaag gcacggccac ttcgtacaga gctgcatcaa 240

ctcactcttg aaggtcgtac tatttctgat tatttgactg agattcagaa tcttgttgat 300

tcttttactg ctattggtga tccaatttct atttgcgaac atgttgacat tattattgaa 360

gaatgtgtac cagaaaacta tgagtcctct gtttcgcaca tcaataatag atctgaacct 420

ctcactattg atgaaatcaa aactgttctt ctcggtcatg aggctcagat tgacaaattc 480

aggaagaagg cagtggtttc ggttaatgtt gcttccacat ccactgtgtc ttctgtgact 540

aatccatctc atgctaattt tggaggtttc agaatcagaa tcagagtcag tataaaaaca 600

gaggacgtag cagtattcag tgttacatct gtcagaagtt tggtcatgat gttgccaact 660

gctggcacag gccctcaact tcctatgctc tgctccttat cctatgttgg cacaatttcc 720

caccatgcct cagctttatt ccaatttctt tggagctgct ctgcatttcc ctcttatctg 780

tttatgcagg ctcctgtntc tcaacaatgc cagcagccac t 821

<210> SEQ ID NO 145
<211> LENGTH: 855

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<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 145

tagaattaca ggtctggaga agtatctgaa gactgtagat tcggtgcggg attggattct 60

gtttcatata tacttttta acaacataag ttaatttttc atatagtttt ttatttaatt 120

ttataaatat tttgaataaa accaaaaata tatgtaagtc gttcgtacat aagacgcgtt 180

aaacgtcagt acttaataat aataatatag tgtaagaaac tcaactgggg aagtgcataa 240

aaaaataaaa gtataaatac aagaaaaatg aactaagaaa gtgtgtactt atgtgctaat 300

tagcaagatc gttggaacaa aaagccaaat tgactggtac tttctcgtta atttcttcaa 360

ttttcattgt ttcgttaaat actagtggca tgtccgtcaa aagtcaaaag ccacatattg 420

atgaaattgt gttgttagaa taattaatta attacttgca gagcaaatct cctccacaat 480

ttttcttttt ttctctaccc aagagacttc ctttcaactc agatactctt tgattctctt 540

caggaaaaca tcaactaatt aaaatctaat tttgtctttg atactctttg tccgcggaat 600

tcaccacccc caccttctca atttgtttgc tttctgcttt cttacctctt ttttctcaga 660

tttcatttgg ttgatccttt cttcaattct tcttctgggt ttgtagttgt ttttttatct 720

gacttgtgtt tctaaaatcc atgaaccgta tgtgatttcc agtgtctttt tctttttcca 780

gattcccaga gagaaaaaag aaaaaatcct tttgtttgtg tgagactgta aggatcaatt 840

ggttgagttc tccta 855

<210> SEQ ID NO 146
<211> LENGTH: 1395
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 146

acttgcctga gagtgttgtt gcttctgaac aggctgcatg ttcatcacat ttgaaagaaa 60

ctgttggaaa acctactctt gatgcatctc aacccagccc aactgctact cccagagata 120

ttgaggcttt tggccgatct ctaagaccaa acattgtttt gaatcataat ttctccttgt 180

tggatcaagt tcaatctgca agaaacatgg agactgatcc tagtaatcgg gatgtcaaga 240

gattgaaagt ttctgataat atggtggtgg acaaacagct ggtagattcc aaccatgggc 300

aacagttgtc atatgggtat gataatgtgg tcaaagatgg gtggtcaggt aataattcca 360

tgccatcatc agatcctaat atgctaagct tttcaacaaa gccacttgat ggacagtaca 420

caaatgcatc ttctcaagag gaggttggtt atggtaaaaa aattgctctt aatgttgctg 480

acagtaacaa agcagcctct gttaaaagtg attattctct ggtaaatcct caaatggcac 540

catcatggtt tgagcgatat ggaacttta aaaatggtaa gatgttgcca atgtacaatg 600

cacagaaaat gactgctgct aagataatgg accagccttt cattgtagca aaccaattca 660

gatagtttgc gctttcataa ttcagtagag caaattcaga gtgtcagtga tgctcagcta 720

agtaatgcta gtgaaagtcc aatgcctgct ttagctgcaa ataagcatgc agactctcag 780

ttatcgacac ctgctgttga acctgactta cttattatga gaccgaagaa gcgaaaaagt 840

gccacatctg aactcatacc atggcataaa gaactgttac agggttctga aaggcttcga 900

gatatcaggt ggttgccaaa actaagtgat ttaatgtgct tatttttcgg tgttgctatt 960

gttggtgtag taaaagatcc catgtctcca gttgatattg tgttgtttca attgttttga 1020

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aagaaaacgg tgtgtttcca tagtgtcagt atgactattt taatattgtt ttatgtttat 1080

caatatatca agtatttgtt ttcctataac ttaaaatttc ttactatgtg gcagtgtggc 1140

agaattagac tgggctcaaa gtgcaagcag attgattgaa aaggtttgtt tataataaaa 1200

tcagtctacg catgaatcta taattctata atttatgagt tcactttact ctgtataatt 1260

ataattatag gttgaagaca gtgtggaggt agttgaagat ttgccagcag tggtgaagtc 1320

aaaaagaaga cttgtcttgt actactcagc ttatgcagca acaacttagt cctcctccag 1380

ctgcaggcag gcgag 1395

<210> SEQ ID NO 147
<211> LENGTH: 618
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 147

atttcttata ctcaaatttt tggtacctct ctttccttca ataaaatttc ttcttttata 60

catgtgtgtg tgtgtgtttg gatgttggta ataaatttct gccagaggat ttgaagatga 120

agagtccata agtttgttga ttacttgata caatctaata gagtatttta accggcccat 180

ttttttttctt gggctaaagt gatgtaacat ctaacaagtg ttgaggagat aaaacatttt 240

caaggagttt gattgttgga tatctagagc aattgtaggg ttttattgta ttcatgatgc 300

ttcttaatca ttcaaattgt ttgtgccttt tcatgttata gctttgtgaa gaggagttac 360

tcaaggaaga agcgctttta gtaaaaaaac aacttatttc ctttagtttt attaatgact 420

tgtatgcaga ttggacaaca ctttagggat ggctacttgc ataaagaaga atttaagata 480

gtttatgttg ctccaatgaa ggtatgttga tgcttttgtt tttctttaca tttctctatt 540

cagatttgct ttttgttccc tgcatttgtg tgccattact catttctaag tatagattct 600

tgtcctttcc aggctttg 618

<210> SEQ ID NO 148
<211> LENGTH: 1066
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 148

gtatggggcg attcaggagg tggaatctgc aatacaagag cttgaaggga acaatgaggg 60

gaatgtaatg ttgacagaaa ctgttggacc tgaacacata gccgaggttg ttagccgttg 120

gactggtata cctgtgacaa ggcttggcca aaacgataaa gaaaggttga ttggtcttgc 180

tgacagattg caccagagag ttgtggggca agaccaagca gttaatgctg ttgctgaagc 240

tgtgctgaga tcaagagctg ggcttggaag acctcagcaa ccaactggtt ccttcttgtt 300

cttgggtcca actggtgttg gcaagactga gctttcaaag gcacttgctg agcaactctt 360

cgatgacgaa aatcaattgg tgagaattga catgtctgaa tacatggaac aacactctgt 420

ttcgcggttg attggtgcac caccagggtg tgtggattga cattttcaca tttcagttta 480

ttgttagttt tctgtatgaa ctacagataa ctgactcatt gtttcgactt tcaggtatgt 540

tggacatgaa gaaggaggtc aactaactga agctataagg cggaggcctt atagtgtggt 600

actctttgat gaagtggaaa aggcacacac atctgtgttt aacactctcc ttcaagtctt 660

ggatgatggg aggttaactg atggccaagg ccgtactgtg gacttccgaa acactgtcat 720

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tatcatgacc tccaaccttg gtgcagagca tctcctcact ggactttcag gaaaatcttc 780

aatgcaagta gcccgtgata gagtgatgca agaggtatgt ctcttgacac catttgttta 840

atatgtatga caaaggtctt tgtgctgtgt tttgacttgt gaccttgtct gttgaatttg 900

ttgtaacagg tgaggaggca ttttaggcca gagttgttga accggctcga tgaaattgtt 960

gtatttgatc ctctttcaca cgagcaacta aggaaggtca caaggttaca aatgaaggac 1020

gttgctagtc gtcttgctga gagaggaata gccattggca gtgacc 1066

<210> SEQ ID NO 149
<211> LENGTH: 1052
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 149

aagttcactc ttaactaatg ttttttcact gtattcccta gctatatttc agactggtgt 60

gtgacagtct ttttttgttc atagatattg cggaagcttg aagaacgtgg ggctgaccta 120

gaccgcttgt atgagatgga ggaaaaagac attggggcat taattcgtta tgcgcctgga 180

ggaagggtat gcaactttta ctagaatgat tttcgaagat ttccatcaga ggttggttcg 240

gatgttgaag aaatgctgat taatgttttc ttatcccttc ccctttttag ttggtcaagc 300

aacacctagg gtattttcca tcacttcagt tatcagcaac tgtgagtcca attaccagaa 360

ctgtgttgaa ggtatttcat gatgaagatt tttttttcca gactgctcag ttgacatttt 420

ttcattgatt tcatcacatc aaaaagcctt gatacctaat tctgcatcac cactcattat 480

tttcaggttg atctggtcat tacgcctgtt ttcatttgga aagatcgttt tcatggtact 540

gctcaacgtt ggtggatttt ggtagaggtg aataaatttt catgtgatga ttggtcacat 600

tgtaaattcc ttggtttttg ttaaaaactc tgatctcttg ttataaaagg agaaatttat 660

caagatgaag agaaagactt tcaaagagaa aggaggatga ggaatcctcc taaacaaagg 720

aacaaaacag aaaacaacta ggaagaaaga gataatcaga gaaacaaatc ttcccagttg 780

ctcgatataa ctttcagtga aaatgctaaa gaaacccccc ttaaagcaaa tagatactga 840

gcacctgatc ttataccaaa tcatgtgacg tgctaaagaa acctccttta aaaatactag 900

aacagcttgt agcatatgta gcagatttat acaaaaaatt agcttcttta cttctgtcaa 960

aaccttgaaa accaatcatc gataattgtt tttgagactt aggacacacc caacattaac 1020

tgaaaatgct gaataagtaa tgccagggag gg 1052

<210> SEQ ID NO 150
<211> LENGTH: 742
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 150

tgaaccaggg tattgtgagc attcatgcta tagatgtgta gtttgctgga atcaaattcc 60

tcgagttatt ggtatgagat attttatgat taagaaattt gaagggtttt agcttattgc 120

tttggatgtt aaatataccg tttttagttt ttcaatgatg aaaataagat aattgatgat 180

taataggttt tacttttttgg agcatagttt atattttcta tattagtgca tagtacttag 240

tagcctacca caacaatatg aggcttcaaa tatggtgatt tgcctgatcc cacaatgaaa 300

tagaatgtaa ctttttattt tttttaaaac atagctatag aaagtaactt ttttttattg 360

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aagtatgaac aaaccattgg ttaacaatgc atatattatt atcaactaaa agtgcacaaa 420

tttgtacggg aagtcagtgt cagccatgct tttgaggtaa tgtaactact gagcccaaat 480

gcaaattttg aggtaatgta cagtacacgc cattatagta caatgttaaa tttgctaata 540

ctgtatttaa ttgcatacat atgtaaaagt atgtcgatga aatcttttgt accacttgta 600

ccatccgcgc cttgtatttg ttgaccactc attgatgatt tacctgcatt tttaattatt 660

aggtgttttc agacctaaat aatttgttct tttctttgta ggttggatta taatcctata 720

gtcaaggtgt cttgtatccc tt 742

<210> SEQ ID NO 151
<211> LENGTH: 681
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 151

agaaaacttc tctccgttca tcttctttct actcaatggc atcctcttat caacaaagcc 60

cttccatgaa gcaacaagat gcttccacca acactgatag gagcacccaa atcccagcat 120

ctacagtgac gactgttacg aacagaggac aaagctagct atgctaaact acactaatgg 180

ttaccttcgt aattcttcct tccttcttat ttcattactg ccatatttat aatgatttca 240

acaaaagata atatatggca ttccaaatgg ccataacaga aaggaaaata tcctaataac 300

agagtgagat gaagtttgtt ataacagaaa ggtattttgg ggcaataaca gaattagtgg 360

agtgagtggt ggaatatcct gaagttggtg cccatgctgt ttatcctaca cttgagtcat 420

agcagcgttg ctatcaacga cgcagagaga aaggggcttt gaattaatac ttattcctgg 480

tcatgaagag gaacgcaaaa agtatgcgaa acacaggtac taattccagc ttctcttaac 540

aataaaaaca tatgttttga atgtccttat tgtccacagg tggatttaga gtccattaaa 600

agttggttcc caacacatga tgggagaaca ccctataatt cataaagata ctaccattag 660

ggagtgattt ttgaaagaaa a 681

<210> SEQ ID NO 152
<211> LENGTH: 993
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 152

atcattttca aagagtgtat attttttttt tttaaatcgc tgagttccta aatataatcc 60

aaacactgaa ttgaggagtc aagtgctgtg tgtgtaagac attgcaaaat aagttaccac 120

aaattcaccg aagtttcata gatattgtct tattgttatt tgatcctgaa acatgctagc 180

aggattaata aaaagaataa aaatgttacc agctgcacta gtatagtttt gatcctgtca 240

tcctttctag caatggttcc attccttgaa tacacttcat ctgaatgacc aattttattc 300

ttggcacctt cattcttttc aatggaatca atgttggtgg agctcacacc actggaatac 360

acttcacccg aatgaccaat tttattcttg gaaccttcat tcttttcaat ggaatcaatg 420

ttggtggagc tcacaacact tgaatacact tcacccaaat gaccaatttt attcttggca 480

ccttcatttt tttcaatgca atcaatgttg atagagctca caacacttga agtcagctcc 540

atgatctgct cagactttgt tcctttgtca tcaattgcat cctcagtagt tgtctctggc 600

atatcttcat aagtagagag tttgacagaa tcgctgaaag aaactctttt aatttttggc 660

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gttattgggc tttctaactt agaaacatct gattcaacca ttgacataga aaatctttgt 720

atcggaccag gttggataaa aaaatttcta ccctttgacc aaattttgtt agagtagtct 780

ttggttgtcc tccatctctt cagtttcgtg ctgccactgc tactttggct actggaagag 840

cctttaaagg tattaagttt caattcatcc gtttcgctcg atgtggaatt tggagagacc 900

ctctcaagct ccagaacaga atttggagcc tgccttttc ccccaagatc cttgggtgga 960

tgttgccccc aaagctatct cttactgaag gaa 993

<210> SEQ ID NO 153
<211> LENGTH: 435
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 153

aggcatcgga agatgagaag actgatgccc caaaagcaat tgagagtaca ccccagtcga 60

caccccagtc tacttctgga attgaggatt tatttaaaga ctcaccttta gttacaccaa 120

gtttaactcc agaaaaacca caaaaagatc taaaaaatga tatcatgagc ctctttgaga 180

aggtatgtgc cagtgcttca ataggtttgt ttaaggctga gttacttctt tgagtttata 240

tatatatata tggttagaaa tgctttttaa aatatacaca ttctatattg ttgacatttc 300

ctccttgccc gatgtgagtt attatccaag acaccaaaac aagtgaattt agttgtcgat 360

cgatctctat ccttagatgg gtttttatgt tttggtatgt gaataagatt ttacctgacc 420

cagtaaattg gacat 435

<210> SEQ ID NO 154
<211> LENGTH: 362
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 154

aatacaatta ttcaatgaca atatgctcta tttataaaag aaattgagcc actacactag 60

ccactaactc ctaggtgcct aggaaaacaa tatccagcaa taacataatt tattcaaata 120

ccccacatca cctaataaca atatcaataa cagaaactta aaaccaatta aatgacccac 180

gtcacctaac attccttccc gtaaactgaa tgatcaatat tcagtttaaa caacataagc 240

agtagaatat tatctctgaa actaattatt caaaactgcc cacaccaagc aatttttgta 300

gcttctgaaa tacaggtgct ttgagaggtt tagtaagtat atcagcaact tgatctttac 360

tt 362

<210> SEQ ID NO 155
<211> LENGTH: 652
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 155

attgtgattt tcactggttt gtgagagtgc aaaagaattg ttcagttgaa tgtgcaaaat 60

tgcttggatc agttgaaatg cacctatgaa tttgtatttt tctttttttat gacaaagggc 120

atgtagaata tgattatatt ttgtttgaat agtgtggggg agcattactg ttttttttttt 180

tttggaaaaa aaaatctgat gtggtagtgg tgtctgattc acatgtggaa aattcttatg 240

gattgggaaa gaatattgat tgtttccttt tctcacagtg ctggtggtga aagcagtgga 300

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ttccttgcat tcagagttca gggctgtgga taatttggtt gtgtgcaata ccaaccgtgt 360

ccttaaagct ttccagaatg ctcgagttgg atcccatgta agcattcccc ttgatttata 420

taacctttat gcaaatgtac atttaatatg atgctcaatg ctcaagggtt caaggctaat 480

aaacttgtta actgttttga ttgtaattgg tagagatgtc ctttaagcca ttgggctgat 540

cttgatgcct ttatgtattt tgacattttt accaaaaaca taactaatat aggaacccaa 600

aaacttagga ttcgattagg gagaacctaa ggctgcccat taaaacttga gc 652

<210> SEQ ID NO 156
<211> LENGTH: 1180
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 156

aaaataaaat cggagtggct aaccccagaa ttatggttgc cagtttgagt ggctttggta 60

gcctggctgg ggttagtgtt gcttcaaaaa aaccatctgg atatttcaac caaaatttag 120

tagcatgaca caaaagatgc tctaacaaag gcaaaagtga ggtagtgata gttacatgca 180

aatgccggag aaactaacca aacaagagcc aagtaagaag agccaatttt aaaatagttt 240

cccaaaatga gaagtataag ccattgaaag gatccagctt tatagagcca tctttcagcc 300

tccattttga caacagctgc tttaataatg ggggtcaact gccttccctt tgatagtgta 360

ttcgaaagat atttttgaag tagaagaaaa ccaaaatgtt gaccagtcaa tgctccgaga 420

aaagctggtg caccaaataa tccaaccacc aacattgggc ttgaaacata tggtactgga 480

gatgaagata tcaaaggtag gagaaatgaa acaaggaagg agaaacttaa ggcaaagacc 540

cacatgagga gaacactcaa acacgacaag gccaatgaag ctgcagtgac tcaaggacaa 600

aaacattatg ttaggtgctt gacaaacact tcaatgcagt tcaactaatc ataatataat 660

atcaataatc aatgaagagg ggttatatct ttttctcaat aactcaatcc atcaatatat 720

aatgatcttt ctaaaccact gttcatcaac tcccatatca tcagcgcgtc accaaatcat 780

atgataagaa aaggttttac tgctgtcaac cattcatatg ataagaaaag ggttttactg 840

ctgccaacca tactgttggt tgcggttacc acccatcatg tttgatccac gcccagctgc 900

cgatccacca taaggagcac cttgaggata atttggagct ccaactccat agccgcttcc 960

acccccacca cgaggaccac cactgggccc accgggcata ccacttgacc cataaggtgc 1020

accccgccct tgaggaggat atggcccact tccataacca cttcctcctc cttgacctgc 1080

acgattcggg tgattgtatc ccccaccaga gttcccacca gaaggatatc ttcctggccc 1140

accagaagga cctcgaggct ttccataatg atggctaggt 1180

<210> SEQ ID NO 157
<211> LENGTH: 628
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 157

atgcctgcag ttaaccacac attaaagacc acgggagttt cgatggttgt atttgtatat 60

acgggtggga atttttctga ttgtcttaat ttaagattaa aatacaaaaa tacaaatgct 120

gaattctctt gaaaaaaaaa tacaaatact gaattgtagc aaatcaaact tttttttcta 180

cataaaaaaa aacatttttt ttcctaaaaa tgccttttgt ggttgaagat ggttaacaac 240

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catttattt tcagttatgt attcaaatag taaatagtaa tattcattta acctaatatt 300

attcatataa tcaaaacttt acacaagata ctagattaaa atctagtgtg atcattgtac 360

ataaaaagaa taatcgaagc attacactat tttctgtcaa aaaagaaaac aattgaaccg 420

tttcgagcaa atcaaatcat caacatcata tcaagtttat aatcaaagta gatcttttct 480

cgtatcatgt gatttttta tgtgtaaaaa tatgtcaaat taagacaatt ttttttaaga 540

ccctaaatca ataaaaaaaa ttatcgaatc gtgttgggtc aaatttattt attaggaaaa 600

aattcaattt aacttaaatt acccaaat 628

<210> SEQ ID NO 158
<211> LENGTH: 774
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 158

ggaaaaactt tgagacaaaa actaaaacac ttatgaaatt agacaaaaga atgcaatatt 60

aacagaatgc tacaacattt caagaggacc caaacgtaga ttataaggag aataatgaat 120

cctcctattt aaaacagaaa gaaactccta tcctatctaa aacagaaaga acccaatgag 180

ccaaagtggc tcaaaaatgc aataaagtat tccaatattt tcgcatacaa atgattgatt 240

ctttgaagca gccattaacc aagaaccatc atagagacaa tcctatccta tgacgactgt 300

aaagggaaag aggtgctctt gaaaatacac gcatttcatt acaaccaaat gcactactag 360

ataactacat atactgcaca atgcgataaa atttaacact ctttgttcct ttcaaaacct 420

ttaaggcatg taaagagaaa agctccaacc tatgattgga gaaactcatt gttggctagg 480

aaccccaaaa caattcagca ggtgtaccac aaaagtggcc tacctatagt attatcagct 540

tattttagca tgtttatacc tagatgtctc tatttcttta tgaacttcaa tagttcaact 600

accatttgat gaatgtgtcc atgatcatat cataacttat atcacgcaaa cttcagaggt 660

tattatcttt tttgtttctc attgtattct acaccaatga ggtaaaacaa gcgagcccca 720

aacgcatgat gaaacataat catccattgt tgctacttgt cagatcacct cttg 774

<210> SEQ ID NO 159
<211> LENGTH: 637
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 159

acaaagtgct tgcttgaact ttatggacta aaggtaaaat ttattctgga atcttcaatt 60

cttagtgagc tatgtctaac ttcaatgctt atattgcaag cctcgtctaa ctttcacaaa 120

ttgattgcta aattgtttac agtataagta tgacaaaatt gctttctgtt tatgagatac 180

gtccccccc ccccccccct actcattatt ataatgaagg gaacagctga aaataattta 240

tagtaaggaa attagttgat ttttttttt acatttgttt gttgtcgact gcaaccgaga 300

aatgacaata attgtgtcct tgttggcaag gacttctttt ctggcagctg gcagagttgc 360

agatgaaggt tcggtctgat gtgagttctg aatactggct caatgctaag tgtgcatatc 420

ctgacaggca attgtttgat tggggcatga tgaggttgcg ccgtccattg tatggtgttg 480

gagatccatt tgccatggat gctgatgatc aattaaagaa gaaacgggag gctgaggtaa 540

ctttcttttc ttcttcagta atatgtattc cccctctccc cttttgtggg tttgaacttg 600

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gtttccatat catggatatc atagactata gttacat 637

<210> SEQ ID NO 160
<211> LENGTH: 1040
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1)..(1040)
<223> OTHER INFORMATION: unsure at all n locations; n = a, t, c, or g

<400> SEQUENCE: 160

aacctccatc accatctggc tctttctcat agtgtagatt tgctgtagca aaagccacat 60

cctcaatcct ctttgcattc tcttcagcct tttcctggtc caaagttcca tacttctgtg 120

tgaaaatcga tttagtagtc agattgttgg tcatcctctc cacaagggtc tgcctagtgt 180

tctgactagg aggccataat ttgattgaaa atggtctcgg ctgtgaattc agctccatgg 240

caatgaaacc tacaagaact gcaagtgcaa gtatataaat ggaatatttt aggatacata 300

acaagagtaa aaaatagttc aagcagactt gttagagaaa acaattgtaa ggcaatgtca 360

ttcatagatg catgtcctca atatggtatc agcccttgtc agacagaata aaacatttta 420

caagccctta acacaaattt gagttttgaa tggataaaaa aaaatgtttt acaaaacagg 480

ttagttaata ggagcagaag taaaagaaat cccatccaag aaataattgc tataacatat 540

aaacatatat atacacccag gcccnnnnnc ncaanncanc acacacacac acacacacac 600

acacatatat atatatacac acacacgtaa agtggattgc aataataaag taggggcatg 660

ttcctttcca tttcaatcat atcatgttaa tgaaactaat aaaaacttca aagcatgatg 720

aaaaaatgaa aagggttagg gagtttataa aggaaacttt gcaaaacata ccatgaatgt 780

acgtacgagg ttgtttcctc tgaagagaag agaacactca caaaaccgtc gacagtaata 840

aataaccgac aatcaactta gtttggttca cccacaaatc aaacccatcc taataaaaat 900

cttagcttta agctcgaatg caacagatcc gagactgcgc aaagatacaa actttaaaca 960

cgaatttgaa aatctttgga gaaaggggaa ggaactggga acagggtaga ctgaaataaa 1020

gagagacaag tttgacaacc 1040

<210> SEQ ID NO 161
<211> LENGTH: 845
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 161

tgcatgcctg cagcttgctg ccaaactttg ctacatttgg tatgattcag acagaagaga 60

atcatgttag cttctgtact atgtagaatt gtatggttat tagtgggttt tgtcaagagt 120

taacagtgaa ctgcaaaatg gagtgtttag agggatgcat tgtatataat atttacgtaa 180

caagtgtggc ttcccagttt tcagccatca tgatatcagc ttaagtgaca taggcgcaaa 240

acaatactga tttcatgcta atgatcagat tttcctcgtg cagtggacaa tgctaaaaag 300

actgatccca aagctcaggc cttgaagact gctatggctg tgattgtgaa atcaggatgc 360

caagtgttta agaaaaaaac taaatggacc aggacattac tgtgacatcg attacatttg 420

gcaggccaaa gacattgctg taaatttgaa actgtttggg atattgctgt aaattttgga 480

ctgatattga acgtttgatt ctgaaactgt tttggacaga tattgctgta aatttcggcc 540

-continued

tttgaggaaa aatgttttgt tgctgcaact gttttttgat tctgaaatat tgttgatatt 600

gctgtaaatt cttaaactgt gttgtggctt gtttacgttg tgtattgatc aggtttgaga 660

aaaaaacata atgaatcaaa gaaatttgtc aatacatgcc aaaaacattt gcgaatgcag 720

taagtctggg taaatcatgg tttcataacc accacgttag taactgtgta aatggcaggg 780

actagaacac actaaatttg ttttgtacaa ggattaaaaa cttacaaggg gtcaaaaatt 840

ctaaa 845

<210> SEQ ID NO 162
<211> LENGTH: 631
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 162

ttgcctgcag ttctgcacat tgtaagcttc tggattagaa ctgtttgttg gaagtgatag 60

ttgtttatta agggtaatga gagttcgaga tgttagtgtt attgttgttg ttaaaatgag 120

ttttttataa cttaaaatga gtcttaaaat gaatttttgc ataagttaaa aatcttttaa 180

aaatctatga gagtttttat aaattatttt atttagctta tcttcattta atttttttc 240

tcttaaaagt gttttagaat aaattcattc aaataagtaa ttattattgt tgtcgatatt 300

gttattgtta ttatcatatt ttgttttttt ttttgggaag ttgaatatca taaactgatt 360

taaaaagaga ggccttggtt gtaaaaaacc ataaacttac gtcataggtg tgcgaatatg 420

ataactaaaa aactttcgag gagtgacttt tgacggtgaa attgggaaag aaaacaacat 480

actagagaaa ttcatcaaca tactttatct tatttataat ttcactttgt tacaatacat 540

tggggttttt ttataatttt taatttttttt ttatcgaatc tttcaatttt atgtgccctt 600

tactgtttac cataaaaaat atccccctac t 631

<210> SEQ ID NO 163
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 163

aaccaaactc ctttttgtgt tttacttagg cagccaaatg cttgggatat cttagattga 60

aaagaagagg aatttgtaac ataattacag tcaacaaaaa taccaatggg tgctatctaa 120

tcactaggta aaaaaattta gaaaaaaaaa ctgataaaaa cagcaaaggg acacaattca 180

attgaaatat ggaaactgta acacattatt taagttcata cttaattagc aagtttgaca 240

aattgaatat ggagagctag catagaaatg atatcattca ttaaaataga aataaataaa 300

taaatagcaa ggacaagttg atcttaaatt tttaaacagt acaacaataa gcactaagta 360

gaccaagaca ccatgatagc gataatatca ccagttcaga attagagtat cagtcattga 420

atatgaaaaa tgaatgtca 439

<210> SEQ ID NO 164
<211> LENGTH: 543
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 164

acgaagaggc aaagaagaaa gctcgacttg ctaggtttgc acctgcttcc aaagttgatc 60

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ctcaagaaga agataagagg aaagcaaggg cacttaggtg ggttcatcat tcctctcata 120

atttgtttct cccaattcat attgtttaca agaatcaagc atgcatggtg tcttattagt 180

tattaggtct ttctgttttg ggttcccagg tttgcgaatc cgtcgtcaac ttctatagct 240

aatgttaatg gcgaggcaaa gattgagccg gtaagaccct tttggtcact ttcaatgctt 300

tgcgtcatac aaagatgaaa aaaaaatgta tttttgtgtt gactgttgtt ctgttgtgtt 360

tcaaactaga aggctgctat tgcaggcaat gctggaggag ggacctgaat gacaggtcgc 420

gtctttaatt tgtaggaatt tttcttgtaa gtcaattatc ttttgctctt gcttattacc 480

ctttgctttg catattgcat atctgatttg tgatgttatt ctctttttt cccctcaact 540

ttt 543

<210> SEQ ID NO 165
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 165

ggcttattga cttgatcagc tgaaagatga actttgcaag gagaatttac agcttgcagg 60

tatttaattt cttttattta atggtcggcc tataattaaa ttgtagtaga gcttctcaaa 120

ctattgcctt tactacagag gaaaatcttc aaaaggaacc tcgtatcatg gaacttagga 180

atcaagtaag aatacaatcc tatgattagt atgctttttt cttttcaatt tattgctgac 240

tactgacttt ttcttcttcc tcccatggaa acagtgtaga ataattcgga caactgagtt 300

agctgctgct aaggagaaac taaatgagct tgagaagcag aaagaagaca tgttgaaatt 360

gaattccgc 369

<210> SEQ ID NO 166
<211> LENGTH: 821
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1)..(821)
<223> OTHER INFORMATION: unsure at all n locations; n = a, t, c, or g

<400> SEQUENCE: 166

acatgaaacg catttaaccg agtatgttac cagtattcat tcattctgtc cttatacgac 60

ttgctgcgaa tcctttgttc ctttataaaa tgaatcgtca tttaattgaa atattggggc 120

ctaatgctaa atttttaggg ttttataatc cacattcttc gggttcgggc aagaagagag 180

agaagacgca attttgaccc tcaatttcac agacctttaa tcattcacgc gattcttctt 240

ggtaactccg ccttcctcaa tccataatct gcttttataa tttatttatt tagtttttat 300

tttgattttg gcttgctgca agctaattta cgctcttcag ttcaatattc cccgttcatt 360

tgttgcagaa atctggtttt ggggcaatct ccgtatttcg atattctggg tatgtatcaa 420

aactgcacct ttttcccttg tatattgttt tgaaatgctt cttagtttta atgactatac 480

tgagctttta cttcagtttt ttctgttttt ctgcacgcct tttatgttat ttttcacctt 540

tgaggtctct ttgaaattta tgtttatgtc gatttgtgca atgattattg gcaaaaaatc 600

aaaaacaaaa atgacttcaa ttcctcatgt ttcagcctgt gcttattaga gagagtagga 660

aaggtgaaga ggggctgaaa atggaatgca tggaatgaat tttcattgag atggagtatg 720

-continued

gaacanagca ttatgctttc ctcttacttg ggaggaatga acattatttt tgggaaactc 780

atattagaat aacctgcccc taatttacac ttttttggga g 821

<210> SEQ ID NO 167
<211> LENGTH: 848
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 167

gttgtgatat tttcttcact ttttcttggt tttcgatatt tagatcaaag taaattttta 60

tactgtccat ttggtttgtg gcatctaggc atctggctct tctgctgtta atgttagtcc 120

tgtcaactgt aaagtagaaa ggagctcacc agtcaggcct tctccaattc ttgtatgaat 180

ttgtccctgc aaactctgta tgcctgatta tgatattagc atgatgacta tgatatacta 240

gtcatagctt aacaattaga aattaatatt taagtattat aactaatgct tcatttcttt 300

taatatttac acaagcatgt tggaccagct tgttattttc ctaatttctc ctggtatcct 360

taattccact atgacatacc cttgcatacc gtggaggact taacatcttt tggacatctt 420

tattatttga tgtctgtatt tctttgtgaa attatttggt ttaattaatt ttttgaagtt 480

actttatagt catgaattta tactgcatct taatacttgt tcacaactca ttgattggtt 540

atgccgtttt caacgaagaa tggagttgat cccatgggtc gaaatgtgga gaaacctaga 600

actgtggaag atggaataga taaagctaaa ccatggcagc tgtctgaaat tgtggatgct 660

gtccaatgtc ggttagttac aacgcctgac agtacagatt cttccagcaa ggtttgttga 720

ttttatgaaa ttgagattgc cattttctat tgtaaactgt gtactgtgaa ctgctttaac 780

tctaaagtca tacatagggt tgttcgactt ttatatacaa actctggtgc tggtcttttg 840

gcacttgg 848

<210> SEQ ID NO 168
<211> LENGTH: 825
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 168

ttccgacttg caagaaggtt ttgtcatgat gattgacgat ggaagaggca tgttacgaaa 60

tttaaatttg aatcgcaatt ttgaaaggta atgctgagca aacaaaagaa atacctttat 120

ttctccattt ttccaatttt aattattttg catattcaat accttatgtt attttttctg 180

agtttttctc acaaatattg actgcaagtg ttttgtagtt tggttgggaa tatttttttt 240

tcattgacct agttttgttt ggtgcagaga gattggtcta atattgaatt ttttttattg 300

gtaattttgt attgttatta aactattcag agattttatt gtgtaaaatt gtatgttgtt 360

cttatcattt ggttgaagtt tacttattag tagtttctta tgttataaac tacaggttct 420

gtaaatggag gaaattacaa agaattggca gcatgaccag caaatagatc atcattggta 480

attaatcatg ttgatgggta ctatatatga acttttttgg gactcaccaa atttttgtct 540

acaggtaaat tgatctatca taaaaaagat ttgcaggtaa gagtctacgc atcttccgtt 600

tggtccttga gagagacatg gtttcatcct ccttgaaata tatttagacc cttaatttta 660

tgttaatttg cgtttttttg tatgctacct atttttactc atttgtctcc attttactga 720

ttaactaata attttttttt cttattcaag gtacactttt attattttat gatagattag 780

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acaatttaaa ctagtctaat gcctaacatt ggctgcaggt cgact 825

<210> SEQ ID NO 169
<211> LENGTH: 953
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 169

ataatgaaaa gaaagaaccc ggctggtggt tagttgcatg cacactcttc agtttaatca 60

ttttcagttt cattgtcttt gtcaaaaaat aagttttagc ttcttgagtg ttggtttgat 120

taaatttcga gcatccttaa tccttatgat tctatttttt actttggcag gttcagtggg 180

gatttaggac aactgagatg tactaaaatg gataaacaat tatttggaca ctaatgaaat 240

cagtatttca acacgtgtct taggagatgg tggactagtt catacgaaga aactcttatc 300

atacaatatg gtttgaaaat tttcttttag aaaaaaaatt gcagggactg tctgtactgc 360

taaatacata ttcttatatg ggaacaaatt ctaagaactg agtatctttt cctagacttg 420

tttctttgtt tgttatgaaa ttaatacttt cctggagctc tacaacatta ggaagttgat 480

cctcgttaat gtataataat atgattgatg aaatattttg aatgttgaag ttcaggaata 540

gaaaaacaaa atcaggaaaa tatatttaaa ttttcaatgg atttaatatt caagacaact 600

agatatttta aatttaaaat taattaaaat atagatgtaa ctttgttttc ggcctaactc 660

aaccgtaata aggcaaaaaa aattggtcgt attttggcac caaaaccact tggacccgcc 720

tgattcaacc cataatctgc aacaaccgac ccgctgaaat tgacggtcaa ttctgtcata 780

aatgggccta aaaataaaaa ggatgtggat tggtatatca agagcttggg ctcggagatg 840

gaaaatattg gttacaacat gagagcctat gctatttgta gcttccaata acccctgggg 900

aactgcttgg gcacccagca gttttccaaa ataacatatt agctttttc ttt 953

<210> SEQ ID NO 170
<211> LENGTH: 598
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 170

ggacgtaatg tgaatagtta cgaacaaatt acattaagag taattacact aacttaccaa 60

acataatgtt ttgtaactat catacttaag agttttggat tcgaattatg aggtattcca 120

caagtttaga ttcctttaaa tcagttgaaa ctaatttagt ttgaaattta atcttacata 180

aaaaaaatta tcctatccaa gacataatta aattatatta aaatgagtta tttatgacac 240

atagacattg gttaatgaat taaaaatgac tttctttaag gaaaaataat tttttttat 300

tattattata aagtaccaca aatttatttc cttcgtaatt tttaaagtat cttattgtat 360

tttttaataa aataaaatat ttattacttc cttgacatag aactctaatg gctgattagc 420

atgacccatg gtttattaca cttcaagtct tatttttatt taaacataac ttccttttac 480

atacaatttc tataccatta tttattgaaa ataacaaaga taaataaatg tcctttcctt 540

aaaaagaaca agtggtgtaa taaatcctaa cgctttgttt ggctgagatg acagtcta 598

<210> SEQ ID NO 171
<211> LENGTH: 724
<212> TYPE: DNA
<213> ORGANISM: Glycine max

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<400> SEQUENCE: 171

ttgacagctt gctatgcctg cagtgcttac atatgcagtc acaagagtgg gaaggcaata 60

ccccctcccc cgtttttttct atttagtgtg gttttattct cttgtacatt cttcagtgta 120

ctagcctaca acattttagt tttgaaattt aagttcaact tgcaaatttt tgtggtccgt 180

tcaaaaatta taatgaattt tgctgattta tgtttattag actggtgcaa tttcttaatg 240

gatttctctt gtctactgtt tcagctatga agcttgggtc atttataatt ttctgtcact 300

gtgtctggca tgggttggtg gtcctggagc agttgtaata agtttgagtg gtcgagttct 360

gaagccatca ttttgtctga tgacttgttg ctttcctcct ataccgctgg atgggtgggt 420

ttgtatctga ttcatatttt tggatgtgcc tgaagatagt tatgtattcc ttgaaaacta 480

tcccctgatt tttctctatg gaggtttttt ttaattacct aacttttttgt tagttgaaag 540

tactaggatg atacatttgc cacacaatat ggagatttat ttttatggat tattggaaaa 600

cgacctagac atcctggaga tgcaatggat tttagtagac ttctaacatg gtggcatgac 660

attatatcat aacttatatt cttctctcat ttctagaact tctatttcag gcgtttcata 720

cgta 724

<210> SEQ ID NO 172
<211> LENGTH: 698
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 172

ataccataaa ggatgtcaac ttagcagcaa cacacactga ccaacaggat aatacataag 60

tttggcattg ggcaatcaaa aaaatgaaaa taaagctatt aataacagca gtgtgtggtc 120

ttatttccag agttaataaa aacccaatgc atttcattaa atgtgtcatt gaagaaacaa 180

cttctggaac tcctccattt ataaatacat caaagcagtt acacgacatc aaattggtct 240

ttgaaggaaa atgaatgcca caaattatca tcaaagcacc aacctttgga ggaccaatct 300

aaccttgcaa atatctttaa ggatcaaaat ggatgatatt ttatagatga taatgaaata 360

tataacatcg tggagatttg atgttgtaag ggatgagcta gcagatgaat tgcaatcgac 420

caaaatgaat tcatgaaaac attagttgga accttcagta gttcaaggga aaaaatcagt 480

gacacctgtg ctcagttaat tgattttatt atgcattcta aattcatatg cacattaaga 540

aacatagcca cttaaccaat gaactagcta tcctagttcg gaagtattta tacttcaatg 600

gcaaccaact ccttcacatc acataactaa aaaataatac tcatgtaacc aaaaaatagt 660

tgcaaatcag gaataaaaaa tgtctcaaag gcaataac 698

<210> SEQ ID NO 173
<211> LENGTH: 673
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 173

agagtcgacc tgccaggcat atagaaaagg aactcattca caaccttact cattttttgtt 60

ttttttttttt tgtcaaaaat gaaaaggaat ttctgtgcgc ttataatgta ctgtaactct 120

aaagaaatgg tattgttgaa acgtatggag aatgggggaa aaaatagcat tcaacacttt 180

ctttttgttt ggatgagaga gaaagagaaa aaaattaatt tttctttttct agacttatct 240

-continued

ttcctcccta cttttatttt cattatctct tcaacaatta agagaaattc ccaattttta 300

agatgttctt ccgtaactat tttctttctc ccgatccaaa aatagggcta aagaagtacg 360

aagaagagca attcatataa aaaagcattt gatatagcaa acagaatatc ttccttgata 420

cctggtaata tgcacattag aagtagtaaa tacactctac ataccttctg acggctctgg 480

tttatatctg gcagttctat acttctgaaa tttaaaaata atgtgaaaag cattagatta 540

aataaattga catacaccca taagctattt aagaggatga taaatcacag atgtacctgc 600

aagtggcttt ttacatgata gatagtaagg ccctcaactt tcattagatt caacacaccc 660

tttggagtag cct 673

<210> SEQ ID NO 174
<211> LENGTH: 868
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 174

aaacgctagt gttcttgcat tcttacacta cgagaacaat cctcccatac ttcaccataa 60

ccttaaatct gcctgcatct tcctagatga tgactattct gtcaagattg caggatttgg 120

tctgatcaac tccaattttt actatggttc tcacttacac aagaactatg aagcatttga 180

catctgcaaa aatgatgttt acgatatggg tgtgttgctt cttgagatta tctcaggctc 240

aaatcagttg gattcaccaa ctttggcttt acagcatgta agggctggaa aatttgaaga 300

aattttggac ccatttcttt gctatgatga acaaccacat taccgccaag agcaaatgca 360

aataattgca gatctagcta caaggtgcct gttatttggg gtagatggaa ggctaggaat 420

gatagatgtt gtgagggagt tagtacacat gactaaagaa agtcttgatg gaggaattat 480

gaaaggacct gcactggagg agacattctc aaattcaagc cttcttcaga tgatatcaat 540

gtctcctgat tctatgagtg tcccttgaat ctttatgtcc cagtcagttt agtttgtcag 600

tcccttcaaa agatgataaa caaccacaat tgtatgtgtg cactataagt ccccagccac 660

tgtacattgg ggaatgcatc caatattctg gttctgacat acttcactaa ggtacaaagc 720

aagtgtattt ggtagctact tcttaataaa tttaatcaac tgctattgtt aatgtgtggg 780

aatcattttc aatacagagg ttttttatg ggtatatata tagttgatga aaatcttcgc 840

gaaaattgta atgtttaatt tattgcat 868

<210> SEQ ID NO 175
<211> LENGTH: 564
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 175

aaaaaataat tatacttgac tgatccatat caagccaacc atcaaataag ctcacaagaa 60

aaatcaacca gcaacctcaa ccagacataa aagtaatgcc tgaatcacaa gcaaaagtac 120

tcaagatcaa cctgatactc agcaaattca actgccagtt ccttgaacgc tttgtctgct 180

ggttgaagta acttatgggc ttcctgaaat tcgacaagaa tgggatttca tggaagaata 240

tgcaaaaact atcagcacca agtagaacaa ataaaacaat attagatgaa tcatccacaa 300

catattatgc agatgaatat tttacatatt tgctaatata aatcaaatgt caaatattac 360

atctatgaaa gttggtatcc tttccatttt catcactaga tacaatggga cttgcaaata 420

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tttggaatga atctcatccc atgtcaccat ctatcaaggt tgagcttata acaaggaaat 480

gacataaata acaattgata tattttctat taaaaagaaa agaatcaaca attcaacaac 540

caaattgaga caaatacctt ttca 564

<210> SEQ ID NO 176
<211> LENGTH: 780
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 176

agaacatttg ctgctgcttc tctcagttta tccatcttct ccacagcttg cttacaaatt 60

cctccaacta aattggtagc aagattttca ttgaataaaa aaagctctcg gttgttctta 120

agcatgctat caatcgaagg atatgcaata ggttcaattt catttccatc tgatcttcca 180

gacaaacaaa ctgacttgtc tatcttacag agcatgtatg tacatttttc taggccatcc 240

aatgcagcct cacgaaccca agaacctaca tcacctctat tatcaacaga ataatcatca 300

agagctttaa ataaacttat catcacctca ttctttatca gaataaacag ggaaaaatca 360

tcctcaacaa aagaggtagc agtatcttct cttccattaa ttaatgtttc acacactaat 420

gtgagccctt tgacagcatt tactcgtgct tcagcatctc tgtcttcagg gttttcctgc 480

acatgggaaa acattgtgta acacaatcat tgaacctaag attgtataat atatagcatt 540

tgcaatgtgg agcacctcaa ttttacaaga gccacaaagc ttcaaaagca catttctcca 600

ttgactggct aataactcat atggcaaaac acctattgcc aatgcagatc ctctccttac 660

agctacattt ggatcagtca acatactgga agtacctttg cttgtcacca tcactttatt 720

acctttatta ttcttgaaag ccatggccaa taattgccac ccggattaaa agtggttttc 780

<210> SEQ ID NO 177
<211> LENGTH: 1536
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 177

ttcggactcg tacccgggca tctctaaatc gacctgcagt gcaaacaatg aaggttatct 60

gttggaaaat tcttcctgtt tcatacatct gtttggatca tgtgaaaagt ttgtgtggaa 120

ctacataatg aagcactagt agcatcctga gatattcttt ggatatagta attagaaata 180

taataataag aaatgctagc tacacacttt cagaaatgct cttttcaagt cacactcttt 240

actattgggt gcattgtttt gtgggtactg ctccctttct agtgggtcat gcataaattt 300

cacccaataa caaaaggtgt gttgctactt gctagccgtt ctcatacata atatatggcc 360

ataaattatg atttcctcat tcacacaact tgtgctactt atatttgatt tcatgaacat 420

tttggattcg acacagtgca acatgcaatt aacaagtatc tgtaattgca ttttctttat 480

tgacagggtt tgtttttacc ttcagtcatt tctctagttg ttcctctggt tctgatctcc 540

ttgactaggt agagactctt cttcctacac tgcaaaagtc agctgcaaaa gctgatttga 600

atagtaagat ttagcttaac atataatgtt aggaacttgg caatttctct attgaagtat 660

cctaaaaaat agaaagaaaa gaggaaagat ttgaaaatat gatgaaagtg ttattactga 720

ataggaggta caataagcct tccgaggaca atttagatga tgctagttct ttacttttt 780

cagtggagtt aatgggaagg aacaaaaggt ctctggatgt ctttgcctct gaaccgattg 840

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ctcctcgagg gcaacttgtt ttctcagtga gtttaggagc tttgattttt gtcccagtgt 900

tcaggtccct cacaggttta cctccgtaca tcggaatgct gctcggactt ggcatgcttt 960

ggattttcgt tgatgctatc cattatggtg aatctgaaag gcagaagcta aaagtgccac 1020

atgctctgtc aaggatagac actcaaggag cactattttt cttgggaatt ctattatccg 1080

ttagcaggta gtgcggaaat atattttaat ttttatgctg tgataagttt tggacaataa 1140

ccatgtatta atgcattaaa aacaattata aaatacatca agtcatcgac aaaagtgtca 1200

ttgtcccttt gagtagtagg gcatttgcta tgacttaata ggtctgatat ccacaaagtc 1260

taacattctg gaaagatgat atattacctt gtttttacct ttttcctata ttatgagatg 1320

catatattgt tcttttgcat gaactgtgat tacatattct tttgctgaca tatctttaaa 1380

taacctagtt acttatgtta gccggttgta tttgatcaat tttaaccatc atgttcggca 1440

gcctggaggt agcagggatt cttcgggaaa tagcaaatta ctttgatgca catgtcccaa 1500

gatgtgaact gattgcaagt gctattggac taatat 1536

<210> SEQ ID NO 178
<211> LENGTH: 727
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 178

tctacatgtg ggctttacct cagacagggg agccaattca attaatgttc actggtacac 60

aaggaaacaa aatcttcacc atgtgagtct aattctcagc ttcattcact actactctat 120

tatctattca ctatctactc tgctgaccaa ttttatgcca cgcaggtttg ggatgttaac 180

ataattgaga cagcagaaga aagattctat gactccaaca tagacgagtt caccaatgcc 240

attcaagaga atattacggt attttatgca gtagctttct attatcccca atccatggaa 300

ttacttcaaa gttagagatg cttactccaa attttctgaa acagaaaaca tggtccgatc 360

aagtactagg atgggaaacc tgcgattcta aggagactgc atgccctgat atgtatgtcc 420

ctttagttct ttatttatgc aaaagtttat tccttcatca ctgaaatata tgctgttgaa 480

atattggaac ctgattcatt agttgattta catatgttgt tgaaatataa ttgtttaaca 540

aacttgggat ttttttcaga tacgcgtctg aaggagttca agcagcctgt caatgggcat 600

ataaaggtgc tcccgaaggt tcagtgctag aaggtaagat aaaatgattc tgagaagtta 660

aagagtttca gtcacttttc agattttctg acaatatcat gaaataatac tctgcaggca 720

tgcaaga 727

<210> SEQ ID NO 179
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 179

aatattgcat cagatttccc aatgccaata agatcaattg tgactgtaaa agggtgctgt 60

gctgtagctt gcctctactt ttacaaattt gttgtcttca actttgtcag atctttacaa 120

aatcatcctg tcgattattc tattgtacta atttgaaaat tccaactctt gttaactgac 180

ttttattttc cattctattg atgtttcatt gaaaaaattg ggaagtccca tgcattaatt 240

ctaaattaag tgaagttact tattgtagat gattgcgaaa attaggcaga atcatgtgat 300

-continued

tctgattgta cgactataat taggatatgc tattatttcc tttcttagtt acaacagtta 360

tagggatttt ggttcctgat ttttagctct aaattagtgt acaaaatcag tcttgtaacc 420

ctatttatac acaccattgc acctttttca aacaatagaa aaatacagtt cattttcta 480

tatggtatca gagctcgatc tgatacttcc ctgaacccag tgccgggcct acaat 535

<210> SEQ ID NO 180
<211> LENGTH: 1201
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 180

aagacttgtg ggtagctgca ctttctcatg agttgctgct gaggcaaaaa tccagggcta 60

ggtggattaa aggagatatc atcaagaagt tttggcccac aattaagtct gatatcctgc 120

gcttcttgga cgaatttttt gttaatggac attttccaaa aggaagcaat gcctctttta 180

ttgcattgat tcctaaggtg tctgatccgc aatcccttca tgactataga cctatttccc 240

taataggttg tgtctacaag atagtgagca agctattggc caatcgattg aagaaagtta 300

tgcctaccat tttagatgaa cggcaatcag cctttataag cggtaggcac ctgctgcaca 360

gagtcattat tgcaaatgaa gtggtagagg aggctaagag aagtaaaaag tcatgcctag 420

tgttcaaagt cgattatgag aaggcttacg actcagtatc atgggaattt ctgaaataca 480

tgatgaggag gatgaatttc tgccccaaat ggacacaatg gattgcagga tgtttgtctt 540

ctgcatcagt ttcggtcttg gtgaacggga gcccctccgc tgaattcaaa ccccaaagag 600

acctcagaca aggcgatcca ttagcgccac ttctttttaa tatagttgct gagggtctga 660

atggcctaat gagacaagct gtggagaaaa atctattcag agggtactca gtgggaagcc 720

ataatgtgaa cattagcttg ttacaatacc ttgcattgtt gggcaaatgg aaattgagct 780

tattccaaaa ccataaagag ctatgggcta aagtgctgga atcaaagtac ggaggttgga 840

ggagtttaga tgaagcatct cgaggttcta atgattcttc ttggtggagg gatctgaaat 900

tggcactcca tcatccgcaa caagagtttg cttttcacaa tggcttggag tggaagttgg 960

gttgcggtga tcgaataaaa ttttgggagg acaagtggac ttgtggtggg acaactttgg 1020

cagccaaata cccaaggcta tatcttattt cttgccaaca gaatcacctt attcagcaaa 1080

tgggagatca caaagccact ggttgggaat gggatttcca atggaggcga cacttatttg 1140

attgtgaggt atctatggct gacaacttca taaatgaggt ggcagcagtg agggtccagc 1200

t 1201

<210> SEQ ID NO 181
<211> LENGTH: 681
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 181

agaaaacttc tctccgttca tcttctttct actcaatggc atcctcttat caacaaagcc 60

cttccatgaa gcaacaagat gcttccacca acactgatag gagcacccaa atcccagcat 120

ctacagtgac gactgttacg aacagaggac aaagctagct atgctaaact acactaatgg 180

ttaccttcgt aattcttcct tccttcttat ttcattactg ccatatttat aatgatttca 240

acaaaagata atatatggca ttccaaatgg ccataacaga aaggaaaata tcctaataac 300

-continued

agagtgagat gaagtttgtt ataacagaaa ggtattttgg ggcaataaca gaattagtgg 360

agtgagtggt ggaatatcct gaagttggtg cccatgctgt ttatcctaca cttgagtcat 420

agcagcgttg ctatcaacga cgcagagaga aaggggcttt gaattaatac ttattcctgg 480

tcatgaagag gaacgcaaaa agtatgcgaa acacaggtac taattccagc ttctcttaac 540

aataaaaaca tatgttttga atgtccttat tgtccacagg tggatttaga gtccattaaa 600

agttggttcc caacacatga tgggagaaca ccctataatt cataaagata ctaccattag 660

ggagtgattt ttgaaagaaa a 681

<210> SEQ ID NO 182
<211> LENGTH: 802
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 182

ccaaaagaat atccatacat ctcactgatc catcctttcc catagatgtc accagttatg 60

tttgtcgccc agtgagccct atcttcccgt acttcttcgg tttttgaaag ccacaagggg 120

gcaaaaactc gcaggtcatc tatatgaaag gccaaaagcc caccaacttt gtcacatagt 180

tctgggtgtt tcgtgtgcaa tttagccaaa ctgttgtcac aacctattaa gtacctggag 240

aaataatata gaatatatag caagtttcaa tggtgagcca aggaaagaaa cactaatatg 300

aaatacaaga tataagtact cctttaagag atttaatcaa gtttcataac ttcaagaaaa 360

gctctctagc ttgtgcatta aaaaaaacct attccctgat tcatatcgtc gagtgaatgc 420

attatgacca atgtaaatgt agaaaaaggg ctaaggcatc cagaatttcc atattgttat 480

aaattgttaa tagctaaatg taagctgtat tagtccatta gcctccttcc aaaatatctg 540

aaatggaagt gatgggtaaa tgtctagcgg cttacactac atcactaaaa gaaaaggtgt 600

gaaaaagaaa caagtaaaaa attagtgaat acccataata tgctgcaaca ggtcttcctt 660

tctctgcacc aagttcccaa agtataattg gccctcggat tatcatgtct gcatccagaa 720

tgacaaccca atcaacattt tttgccttct tactatgttt aagcccagtg tacaacccca 780

gcagggtttg tttattggca gg 802

<210> SEQ ID NO 183
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 183

agaaaacttc tctccgttca tcttctttct actcaatggc atcctcttat caacaaagcc 60

cttccatgaa gcaacaagat gcttccacca acactgatag gagcacccaa atcccagcat 120

ctacagtgac gactgttacg aacagaggac aaagctagct atgctaaact acactaatgg 180

ttaccttcgt aattcttcct tccttcttat ttcattactg ccatatttat aatgatttca 240

acaaaagata atatatggca ttccaaatgg ccataacaga aaggaaaata tcctaataac 300

agagtgagat gaagtttgtt ataacagaaa ggtattttgg ggcaataaca gaattagtgg 360

agtgagtggt ggaatatcct gaagttggtg cccatgctgt ttatcctaca cttgagtcat 420

agcagcgttg ctatcaacga cgcaaagaga aaggggcttt gaattaatac ttattcctgg 480

tcatgaagag gaacgcaaaa agtatgcgaa acacaggtac taattccagc ttctcttaac 540

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aataaaaaca tatgttttga atgtccttat tgtccacagg tggatttaga gtccattaaa 600

agttggttcc caacacatga tggagaacac cctataattc ataaagatac taccattagg 660

agtgattttt tgaaagaaaa aagtgggatt ttagaactct tcccccaaaa aagaaagaat 720

ggtaaaactt tggaacccaa aaag 744

<210> SEQ ID NO 184
<211> LENGTH: 905
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 184

gatcgacctg caggtatgag tggtgggatt gcttatgttc ttgatgtgga tggaaaattc 60

caatctcgat gcaacttgga acttgtagat ctagataagg ttgaagagga agaggacatt 120

cttacactta gaatgttgat tcagcagcat caacgtcaca caaatagtct gctcgccaaa 180

gaagtgcttg atgattttga gaatcttctt cctaaattta tcaaggtgtt ccctagggag 240

tataaacgtg ttcttgcaag tatgaagtct gaggaaacct ccaaagatgc agtggtgcat 300

gctgctaaac atgagcaaga tgatgaagca caagcagtgg agaaggatgc ttttgaagag 360

cttaagaaac tggcgactgc atcattgaat gagaaaccga gtcaggttag ttttttaaat 420

ttttattata ttctttttat ggtacttgta cctttgatgt tcaaaaaaag cgatttttt 480

aaaaacctgt agattgggca ttcacacttc cttaaagtag ttattgagct attgcttttt 540

caaatgaaat tcaatgggcg gtgttagatt gaattgaggt gagtttgaaa atggagatct 600

tggttaatta cagggaagaa tgcctagaaa ttctactttg agaccgtttc tcctttatgt 660

gaagatggaa agatcttttt agtaaggaaa gtttttttact tcctctttgc tgtaggtatc 720

ctataaatgt tttaaattaa cctagtagat actgtgctgc atttaatgga tgtttaacga 780

tatcttttgg tggggtgcaa gaatagtata gtttgtttat tgcataaatg tgaataacat 840

acaggggaaa taagcaccta gagaaatttt ttcacagttt atctttgttg atgtctttcg 900

aatat 905

<210> SEQ ID NO 185
<211> LENGTH: 863
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 185

tagcaaagag gaagcctttt ttgattccag gcctggttag actcagattg tgaagatgat 60

ttctatagtg tcaatggtgg taagcatttc cttcaactct ctctcctttt gtacttttt 120

tcttcttctg gtagagcatt taaatttgtt tacttgacca ttttgttata atatagttat 180

gacatggatg atattggtta gaggtgaggc tttgtggctg ataatatgtg atggtaaaca 240

ttgtcttacc attattgaca ttatttataa tatgacaatt tagtttgtca tggacaaatg 300

gatattgtat cataatcaga ctttatgtaa tgcaagttga tgaagaagga ataactcatt 360

ttagaaattt tggatatatt gttttacctt tcttatgtag tttctctttc aactattttc 420

attactctcc ccaaccacct tcagctgtat tgtctacttc attttatgca gactttacac 480

catctagagg gaccacacca gttcaccaca cttttgggac cccttctagg aatagaattc 540

atggctctat ggctgaaaca tccccagaaa agaaaaagaa attgttagag ctttttcgcg 600

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aaagtgtcaa agatgaccaa ggtgatgttc atggacacaa agaagtcaag ccaactatac 660

aagatgttat tatgcctaaa tctgcacatt gcactcctta tctctcagag gctaactctg 720

cctgtagtag tgaaaggacc atgagcatga gcgaggatcg ttcatccatt agagagaaat 780

cagtcaagtc tttgcagtgg tgcattccaa gcttgtcttc atgccgaagc tttcgcgaga 840

ggaggccaaa gacgagtcct gca 863

<210> SEQ ID NO 186
<211> LENGTH: 593
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 186

tcgacctcgc ggatttgctt aacaattgat atttttccca gtgctagata tgaaactatt 60

aagttgcaca gtgttttgga gtcttgttat gtttgtaatc taatcaggct atgtttttac 120

tagatatact acactaatac tggagcttga ttattattac tataataaaa gcacttggtt 180

aatttagaat attttacaaa atttgttctt cttttcttcc tttttccctt taatttctac 240

aaaacaactt cactgaacct gcccaattgg agggtgctgc taatagtaag tagattatga 300

attgcttgta aaaaggcatg gatgtaacca tcaaacttgc tctactttat tgcagtatgg 360

ttggtgaagg aagtgaatgc ggtttcaatt tgaacttttt ttggctgtag actggatcct 420

tctttcttca ttctgtttta tgtgactagt atttgttttc ctattgcatt tgtcaaaaaa 480

atcagttttt ctatgtttac cattattatg caggtgctat tgtcatgcag gagatattga 540

gcgtggtctt ccgagttttg agaaccacct aaggcaggac aggtctgttc ccc 593

<210> SEQ ID NO 187
<211> LENGTH: 791
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 187

tcccattcat atacctaggg atgcctatag gtgttaaccc tagaaggaag gtggtgtggg 60

agcctataat cagaaaattt gaagccaaat tgaacaaatg gaaccacaga agcatctcta 120

tggctggcag aattacctta atcaatgctg tcttgacagc tttgcccttg ttttatatgt 180

ctttttttcag ggccccttca gcagtcatca agaggctcac tactatccaa agacaatttc 240

tttggggtgg aaacttggaa ggaaaaaaga tagcttggat ctcatggcag caagtgtgtg 300

ctcctagaga aaagggaggg ttgggaatca aagatatcaa ggcttttaat agagctcttc 360

tcatcaagtg gaaatggttg atgttccagc aaccagatca tctatggagc agaatcctca 420

cttcaaagta caggggttgg agaggtttcg aagagggtcc tcctaagcag attttctcct 480

cttggtggtc tgacttaaga tcaattattc aacatagtag catggctgct gttaataagc 540

agtttctttg gaaactgggc aggggtgatc aaatttttatt ttgggaagac tcatgggtgg 600

gagatggaac tattcttaga gacaaatact cagaattata tcaaatatca tctcaaaaac 660

tacagacagt ggcaagcatg gggatttttg gagaaactgg ctgggagtgg aaattctcct 720

ggagaagata tctctttgac aatgaattgg ggggagcctc agcttttatt gacaagactg 780

caggcatgca g 791

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<210> SEQ ID NO 188
<211> LENGTH: 907
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 188

aattgcatct attgccaaat atgggcatat agcatcagca ccaaaaccaa caagggtgca 60

gaaatgatgc actttgcgtg gctcagcaga ttcaactatc aaggcaaccc tagtgcgctc 120

aagagtttta actagatgct gatgaacagc accaacagcc aggagggagc tcacagagat 180

gcgtttcttt gagaaggcta tcacagatac aaataaatta gatggatgtt cactgtaaaa 240

agtaacttta accaatacaa gcaaaacata gtgcaatacc tctatcagac agcacaagag 300

tggtgtagcc ttcattaatt gcatcatgtg cctctgcaca catcctgtcc aaggcttcgt 360

ccaaccctct cttaccacat tcctttgaat aagttatgtc tataactttg ctgcgccatc 420

ccctataatt catttttta atggcttcca tttcttcagt ggataaaagg ggacctttta 480

gtgaaaggcg gtgacattgc tcctcagtga tttctgtaag atcaccttct ggaccaacca 540

tacattgcat agaagtgact attttctctc taataggatc aataggaggg tttgtcactt 600

gagcaaacat ttgcttgaaa tactcaaaag tgagtttttc tcttttagac atgacagcca 660

atggagtatc atttcccatt gacccaaggg cttctacacc atccttggcc ataggaagta 720

atagcatttc caatgattca actgtatatc tgcatgaata aagcataata taaaaatatt 780

tccttcataa atgcagcaga taaaattgag gaaatattaa tgatggtcat tgcataccca 840

aaagctttca gtggaactaa taaaccatga attcccatat tttccatatc tgcatcatca 900

ttggata 907

<210> SEQ ID NO 189
<211> LENGTH: 568
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 189

actttcactt catcttcagg catatactcc acaccgccat cagtaaggtc atccaaccag 60

ccttgaagat ctgatccaat ctccttggta atagatggat cggatgctcg aaccacaaac 120

ttgcacagca tggttgtagt ctcatcaccc aagtccacat ttctactcac ttcacttgca 180

ccaaatatca tcatgcccaa gaagccacca tgccaagttt tagcagcata acacatctag 240

tccggtaaag gggggagaaa aagtaaagaa ttagtaaatt cattctatgc aactagatgc 300

atataacccc tattgtagtc cttgcttttt agtttttatc ctattttaca atggctaagt 360

ttatcgttct ttaggtacaa atttactgct tctgtccaag tagaaacagt caggtaaatg 420

catacaaggg acagattgaa tagtaccacc actagatttt aataaaacaa ggggattccg 480

ggaatgaaac ataacaactt agtgcatgtt tggattgcca gtagcggcag tccaacttac 540

gttttcaaaa gcatcaactt tgatactt 568

<210> SEQ ID NO 190
<211> LENGTH: 826
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1)..(826)
<223> OTHER INFORMATION: unsure at all n locations; n = a, t, c, or g

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<400> SEQUENCE: 190

aaatgaagtt gatggtgaat atgaagggtc tcactcaact ggttaaggag aaatgtagtt 60

tagcttagaa aactttgtag taagaaatcc cagttccatt cttccttgtt ttgtaataat 120

tttcagctaa catgtttttg taggtgtaaa ttgtcattat tcttttatct ttgtaagggg 180

tatcatagca aaatacagaa tacatagtgc tgcttgcttc ttcttctact tttgatgagt 240

tcctgcttgc tggtactggc attattaaca taaatctagt gtttcttttt tttatttttat 300

tttataacaa actacagagt aacttgacta tgaattctgc gtaagaagat tatgatgata 360

cataaactaa ctaaaagtct gaaataacaa aaatgaacca gttgccattg gatcatcacc 420

tccaagcaca agaggtaata agaacttgat tcatccaacc aagacacaga gccccatctc 480

tctcctctag agtgtaatgt cctcggtagc ttcgctgaag attttttatt gaacaagtaa 540

taaacgagtt cagtggatat ggtgcgaatc cagccatagt aaaacgcgat ctccacttct 600

tcagaagctc gtgacgttcc actctttcct gcccttcaca tgctattaag ttgacaactt 660

ctcgagccaa acaatgctgc tccacattaa tcctttcttt gtgctccctc ggcagagcaa 720

catcaattga ttcanaaata gccaagtagt agttcatcgt ctcaacgaaa cgggggataa 780

tgggannngt gtggtatgtg attcttgctc aactagtgtc acaatc 826

<210> SEQ ID NO 191
<211> LENGTH: 969
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 191

atctgctgct tatactatgg atgagcatcg gagaattgct tgtgcagaaa ttgagcgttt 60

gaataaagat tctgagaagc agcaagagct gtttacacag aaggtatgcc attgttctgg 120

ttcatttgta aatatttttt ggctgatgga aattcatgtg attgtcatta aacttctttc 180

gacaattgac ccttagccat tactatgtat tggtgttact tgcaatgaaa ttatcttgaa 240

tgttcatatt gtcttaaatt gttttttttg tagctgaagg agtctgaaga aaagattggg 300

ggcttaagca aagaaagaga gcaattaatc aggcagagag atgctgctat tcaggaagca 360

aatatgtggc gttctgaact ggcaaaagct agagagcatg atgtgatctt agaagcagct 420

gtagtaagag cagaagaaaa ggttagggtt gcagaagcaa atgctgaaac taggataagg 480

gaggctgttc agagagaatc cgcagcatta aaagagaagg aagagcttct tgcatatgtg 540

aatgtactaa aagcccaact tcaaaggtct agcgtcttat tttctttttc ccttgctttt 600

tattttgtta aattagattt gttggctact tctgttttcc cacctaaaca taaagatgga 660

aaaaatatat atcaatacct agtgaaacag ggaaatggaa ggagactttt gatggtttat 720

ttgtcttttt accagtttat tgagtttgaa tatgtatatc agctacgaaa tgtggagctt 780

cataaaacca aagttgacat agcagatatt tttcttttca acaggcaaca cattgataca 840

actcaagttt ttgagaagac agagtcatgc tcagatacaa agcatgttga ccccactgaa 900

gaaaatgtta taaagcatgc ttgagtgttt ctagagccat ccccgtccct gcaggcatgc 960

aagctggcg 969

<210> SEQ ID NO 192
<211> LENGTH: 1269

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<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 192

aaaatttttg gagaatatac agagagtaca gcatttgaaa gaccacttac tagtggtgtt 60

gcttatgctt tgaaagttct ccactctgat aggatgcatt ttgagaagca gcatgggtgg 120

acaattaaga aaatggaaac tgagaatgag gcattagtcc aagattgtat tcctgaaaaa 180

ttggatccag cacccattca agatgaatat gcaccagtga tatttgctca agaaacagtt 240

tcccatattg tatctattga catgatgtca gggaaggtgt gtcttgctta gcttgctgtc 300

accctagcat gatttacttt ttctaagcaa attgtggggc aatggcttaa actgaaaatt 360

ttacattcct gtcaatgttc ttaccatatt tgttctgcac aagtatgtat aagaaaacta 420

gtgtgaagtc atcagttaga aagacttttt tttctttgta ttttctttat gcaaggttta 480

ggtcatagca ttagatgctt ggagcttttg tatacatgga gtggaatatt agaactggag 540

atcactaaac agtatataat ttactttgaa cagtgaaaat gtgaaagtta aatgtggggt 600

aaacagaatc aactacatac aagagtttta ctcatgaaca tcaataaaat gactctgagc 660

actggttaaa agaaataaga ctaggagtta ctattatcta ttgaattatt tgttaaattt 720

ctcattatct gtctggttaa aagaaaatat tttgttgcat tgttgcacag gaggaccatg 780

agaatatttt gagagcaagg gcatctggaa agggggttct gacatcccct tttaaactac 840

taaagtccaa tcacctgggt gttgtactta catttgctgt ctataacact aatcttcctt 900

tagatgctac accggagcag cgtaccgaag ctactgtggg gtaatcctac atttaactat 960

ctactggtta aaatatgcat ttcatttgtg ctctgatcca cctcccctaa gaagaaaaca 1020

attacaaagt gtaatgtgag tgttgttacc tatttattgg caggtatctg ggtgcatctt 1080

atgatgttcc atcactggtg gacaagcttc tgcaccaact tgccagtaaa caaaccattg 1140

ttgtaaatgt ttatgacaca actaatgcat ctgcaccaat cacaatgtat ggtacagatg 1200

ttgctgacac tggcctacta cacataagca gcctagattt tggggatccg ctacgaaaac 1260

atagatgca 1269

<210> SEQ ID NO 193
<211> LENGTH: 1246
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 193

aacttcctac acatggaagg ccaatgtggc tccatgagag tgaaggtggg cacactgtcc 60

gttcaaattt tcaaaatcat atgaaatact gtgatgtcgt attcgatcca atgctcaaac 120

tatttgttgg ggtttgattc caataaaaac aatgaggtat ctatttcttc ttttttattt 180

aaaaagacat aaataaaagg aaattatcca aacaccaaac ctagtttcaa gggtaaattg 240

ttactgtgcc taggttagga aaatttggta gcatttgaac catttgataa aattttaaat 300

ggaatccagt tgttaaagaa gcttgtgagg aatctgtttt tataatgacc gaaggggggtt 360

aaagaactac ggttaaacaa tgaaactcct ttgtatcctg tgtgtataac atgcataaaa 420

cagtaaggaa atgtttgatt tgattatttt ttattttcat ttttactgaa aacgaaaaat 480

ggtgataaaa atgtgtttgg ttgaatttct gaaaatattt tcagtgaaaa taaaaacaga 540

aaataatcag aaaatgataa cagaaacctc atttcggata aaataaaatt acggtaacaa 600

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tgaatgtaat tttaaacaaa tctaaaaata caaaaagaca agaagttaat atatcataca 660

ttttcagtat ttttatttca tgaaaacaaa aaacaagaag ttaaaccaaa catgttttca 720

gaattctttc ttttgaaaat gaaaacaatt ttcaaaaaat aaaaaaaaaa tgaaaataca 780

aattaaacac acctaatatt ttcgacattt ttactagtac agtagtacat gtaccagtct 840

gatttatttg tttctatttg gaaaatagtt attgcaggaa atttataaaa taaaataaaa 900

aaatcccgag gaaaggaatg tgtggattga attacaaaga taggactcaa attcggttgt 960

acagtttatt gataactgaa accaatgttt acaaggtttg accagagaaa gctagctcta 1020

tctgtggaag cactaactca tgtcatcatc ttacacaaag caccaccaga gacaactact 1080

tctccactat gaagaacctt tttcttattc tccacaagga acgctccacc tggccaaact 1140

attcacaaga caacattctt ctacaacaac cttgtcatac catactgaac aggtccaacc 1200

tttctatgag cagtggtact aatcccacca tattatgagc cttgac 1246

<210> SEQ ID NO 194
<211> LENGTH: 671
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 194

atgctttaat attacaacag atggaagttg atgaggttca gaagcctgaa aatgtaactg 60

gaaacatgat atatctttct aagattgaga atcaagaaaa ggaaaaaggc tacgactcta 120

aatcctctat ggtaaatgca cttcaagatg ccaataatag tgaaaaagtg gagcctagaa 180

ctagtggcaa gaaagggatt gtatgcggag ttgaagtagc aatgtctaaa gaaactattg 240

aatgtcagaa ggaagataaa acgaaggtat tcttctaatg ttattgttaa tttttttct 300

tgatgttgta ttattgttct taacttgtga attgtgatca cgttaagctt cattttattt 360

tcattacttt caattttctt agtatgtacc accaatgatg aattaaagat tttgatccaa 420

tgatgatcct tttgatatat ttagtttagt aagttcaaat attttaggct agcattgcaa 480

tgttttacac agttacccac cctttcccgt aaccaataaa aaaaagtgtg atcacattgt 540

tgtacttgtg tatgtctata tccaaagtct ttatatggac accttaatta tgtggggttc 600

catattgtgg agtgactgtg taatgatttt aagactagtt acattggttc ttttgctaaa 660

ttttgatcat c 671

<210> SEQ ID NO 195
<211> LENGTH: 1137
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 195

aactgcttcg gcatgaggaa cgtgacgagg atgtttttct ttcttgtctc ccctgagctg 60

tttcagacca tgcttaagtg ccggcaataa agcttccata cactcggcaa cagcattagg 120

gtttccaggc atgttaatga tctgaatttg aacaaatcaa gggccataac ttagccagta 180

agtacaagtc tagaagaaag acagattaga tgtctggatc cagggtgtac tagtagttac 240

agcaataaat gcaagatttt ccttaactac tcatgataca gctccatttt gaagccaagg 300

gcacttgtat accaaatgta aatggatgaa actaaagtaa ctagtaataa acacagatta 360

tcatataaaa aagcttcaga atctagattt gagtttcctg aaaatagtaa ctgtttaact 420

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aaaacaacct tactgtaacg gtgaagattg aaaacaatag gtaccttaaa actcaaataa 480

ttaaaatcta acaacagtac aagacatgga cgctttatcc ctcctaatat tctttttaat 540

aaaccagcag ggttttattc atactaactg tgttggtcat ttataatcaa ttttcttatt 600

ttcttataat ttctaaaacg acacttgtta tttcttgtca tcaccctcgt ttaattaatt 660

taagattaaa agggctttct ggctgtttta acaaaccatt ttttctgcat tgaataacag 720

ttaattactt tctcacttgt tactgatagg atattgtaca agtgagagaa taagatattt 780

tcctagaaca gcccataaaa agaaaaagag aaccatgcaa aaccaacaaa gaacatttta 840

aaaataaagt caaccattat tgagatgaaa tattctttta caaattaata agtcatttga 900

gagttgagac actaaattca cactcagtaa ttctatttt ttttagataa caagaggaag 960

agaagattga catatttaca ttcttacatg aaatacttac attgttctat aaagaaattt 1020

tctaagatgc ataaaaagct atagtcacaa agcaattcca attataacac taaaatgagt 1080

tttaaagtag atattaatta gcatttttgc cttaccaagg ttgatcctct gattcca 1137

<210> SEQ ID NO 196
<211> LENGTH: 694
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 196

aagctccttc tttgggagaa gaaactcttt aacgaagtta aggtatggat cttaaatcac 60

caatctcatt cattccattg ctttcagttt tttccacttt taatttttaa tctctgtgag 120

gcaatttaat cctgctgcat tcacatcagt tcttgtatat tctattgtaa ccaacctgtg 180

ctgataattt gaaagaaacc aactgatcag aagtctttta tgccataagt aaaacattgt 240

taaccagtgt ttacaggttt ccacattttt tttttccaac gttcatttgt ttgcaggcag 300

aggaaaagat gcgtgttatg catgatagga agtgtcgcaa gctgaagcgt ttggatgata 360

ggggtgctga ttttcataaa gttgattcaa ctcgaacttt ggttaggaat ctgtccacaa 420

aaattagaat ggcaattcag gtggttgata agatttctat gactataaac aagataaggg 480

atgaagaact gtggccacag ctgaaggaat taatccaggg gtatgtgatg ttaaaaacta 540

accattcttg ttatttgttc aagtcctaaa tgtctctctg ttaatgatgg gcaacactgt 600

atgtaaggat ggatggaaaa ataattccca tatctatgct ccataatcca atccttcaat 660

tccccccaat ccattgaata ttgaattttg aaaa 694

<210> SEQ ID NO 197
<211> LENGTH: 693
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 197

cgctgcagca gctggaaacc aataaccata taccatactt ggtaagagaa taagtgcgag 60

gtggaaatct agaaaaccaa tgggtgttac tttgagtttt catcatttca tggaaactca 120

ttattcaaaa atagaatcat cgttaatgtg ggttggttga cttggttcaa ttggtagcct 180

taactaaatg gtttccaagt acaaaaccct ggcagaggcc tgtggcatgc attgagcttg 240

cttggaatgg agtaacctct cctcccccaa acttctctca caaaaaaatt aaagaaatta 300

gaatcttcag gagttctagg acaacccttc catcatgcta aaaaactatt ttttgaagta 360

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ttgttcaaaa tagtatacca aataccccat gaagctactc aggacagttg taaaagtaat 420

ctaattaaca tgttggaatg cagataaagt cagagaggtg ctgaagcttg atctggagat 480

gaaggatcta gcaaagcagt tgattgctga gcagtctctt cttgtctttg ggagaggata 540

caactatgca acttgctctt gagggagctt tgaaagtaaa ggaagtggct ctaatgcata 600

gtgaagggat acttgctggt gagatgaaac atggtccttt ggcattagtg gatgaaaatc 660

ttccgaatgt tgatctagct acccgtgatg cct 693

<210> SEQ ID NO 198
<211> LENGTH: 738
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 198

aagaaaacat aaagtatatc ggtttgagca tcacttttt gtagaatgcc cacaataaca 60

gtaaattcag atcaaagtaa aaggctgcac aagactcatc agccagagca aattctgatt 120

tgaattcaac ttttacatga ggagtcagag ccaatgcccg tttatagact gagttgcata 180

cagttacagc acctatgact actttattgt ttaaaatttt agtctcctct agctcaacct 240

aaataatatc ctcaatataa agatgacatt gacagtaaat acaaaaagag accaaacaga 300

aaagtcaaga ttgcatacgt gatatactct aaaaaggttg acaacggttc tgtggcttgg 360

catagcatgt tcttgtaatc atcaaccagc ttaagagtac acttctccac aatcgtggtg 420

gtatgcaacg gagaaggctc tgcaataggt aacttactca tcagccatca gcatagacca 480

ataatcttaa ttagatcttg tcaacgagta aacaccattg tactaattgt actaatacaa 540

aagcaacaga aattcttgta aaccttcaat caaattcaat tcaacagaca gagttaaaca 600

aaacccagac taacaaacaa cagttcactt tcaataatag ttaacattca gacagatata 660

acatggaaat aaacaagata acacaccact ttttttctttg tttcccacaa gtatcatcct 720

ttggaagaga caatccta 738

<210> SEQ ID NO 199
<211> LENGTH: 610
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 199

tgcagacata ttgctcatgc catcaaggtt tgagccatgt ggattgaacc aactctatgc 60

catgaactat ggaacagttc ctgttgtgca tgctgttggt ggactgagag atactgtgca 120

gccttttgat ccttttaatg agtcaggcct tgggtggaca tttgatagtg cagattaagg 180

taagttatca catgcattag ggaattgctt aaggacctat agggagtata agaagagcag 240

ggaagggctt caaaggagag gaatgacaca agatcttagt tgggacaatg ctgctcagca 300

gtatgaggag gtgcttcttg ctgccaaata ccaatggtga acttttggca tttattccat 360

ctaagaagac ttgtaaaatg gagctgctaa ttcatgttga atacttccag tgtactgatt 420

gttgtgttag ggaaaagaac tgtgcaagtt gtttaaattt tataggttac agttagagcc 480

ttttttatgg gaagtgggaa ggccaaattt tggtgctgga ttatgtaact gtaatatagt 540

tgacccttcg tgtcaatgta ttaggatcat accaagtgtt caaccacttc aataatactt 600

tgccataata 610

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<210> SEQ ID NO 200
<211> LENGTH: 915
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 200

tgattatggt tttcacacag gactgataat tttttctggt ctaaagagga agttacccga 60

tgactcgagc aaaagtgatg atatggattc caatgacatg attttttcaa actgtaaaag 120

aagtcgagct cacgatgcag aggatttgga ggacaatcca ccagggaata cagcatatga 180

ttgtatggaa accagtagac aaaatagtcc attgtgttca tctatgtccc catgtgcagt 240

tgaaggttgt ctgtctaagg ggtttgcagg actactcaac ttgttcctat gtgtagtttg 300

gtagggagag aagggcttcc ttttgatgaa gctccctct tatagttaaa gaaatacata 360

gaaggttctt ttgctagttg atatctgttg atgtattcat tttgaatggg ctacaattac 420

atgatcctag tttctcatta atattattcg tggcgttgta atttttaaca tcatcctggt 480

gagtgttaaa taactatcca ttgcctttga taaaatgaat agaaatgttg tgttttgctt 540

ctatgggaaa tttgatccat aattcccatt gtttcaatat gtatacttga aattgaaaac 600

taaggacata tggtgaacca gtatattaaa ttttagaact ttgattgaat tttaaaaaaa 660

attattcccg ggtttacctt atgaaaaaga aaaaatggaa aaactgtaaa tggattttat 720

ttattggtat ttatttattt tactgggctc tttctaacaa caacttttag ggacataaat 780

ctaagtacca aattaccttc ccttattttt ttaaggccct gaacaacctc tgaataaata 840

aaagaaattt tttttgccca aatttttga accctcatta aaaaaaaaaa tgtaaatgag 900

actggaaaaa taaaa 915

<210> SEQ ID NO 201
<211> LENGTH: 668
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 201

acttttgtac aagctcatca atgtatatca tagtttttga aatcggtaat gaaccaatgc 60

aaaaaatggt ttaaacccgt atttctttag gagatattag gtgaattgga tgattaagga 120

aaaatggaag gaaaaaatat cacaagttta attcctgcta ataaaattaa tattttaaca 180

actaacattt gctcatataa aaaaccccaa tatttttaa aatttaatct aaagcatttt 240

taagttaact aaaaacatat ttaataagaa ttaaaatagt tgtaaattat tttattaatt 300

attattaatt actcttataa aacatataat ttaatcatta tatcaatttg caatttttta 360

tatcttgatt tcacataatc ttatattaac ttcttgtttt cttttttatt ctagatgtaa 420

acttgttatg aagtgatttt actgggtttt gaccagtttt gattcttcgc caattccttg 480

aacgattttg tagtttattt atatcaaaca ctaaatcaat tcatcagttt tctgggtcaa 540

accaacaaat ttgatctggc atcttataac acaattgttt atggaaaaca catctaatgt 600

gattaaacaa ggacatcacg caacttggca gttaccactt ctttgccttt gctccaatat 660

ttttattt 668

<210> SEQ ID NO 202
<211> LENGTH: 941

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<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 202

caagcttgtt gcctgcagaa aaagcacatg ggatagttgt taatagtttt gaagagttgg 60

aagcagaata tgttgaagag tgtcaaagat ttacggacca tagggtatgg tgtgttgggc 120

ctgtgtcgct gtcaaataag gatgacaagg acaaggctat gagaagtaag agaaactcaa 180

gtgatattga gagtgagtat gtgaagtggc ttgattcatg gcctccgagg tcagtgattt 240

atgtttgcct tggtagccta aaccgtgcaa cgccagagca gttgatagag ctcgggttag 300

gattggaagc gacaaaaagg ccattcattt gggtgcttag aggtgcatat ggaagagagg 360

agatggagaa gtggctgttg gaagatgggt ttgaagagag ggtgaaaggg agagggcttt 420

tgatcaaggg ttgggtgcca caagtgttga tcttatcaca tagagcaata ggagcgttca 480

tgacacattg cggatggaat tccacactcg aagggatttg tgctggcgtg ccgttggtaa 540

cttttcctct gtttgctgag cagttcatca atgagaaact tgtacaagtg gtgaagattg 600

gcgtgagtgt gggagctgaa tctgttgttc acttgggtga agaagataag tctcgggttc 660

aggtgaccag agaaaatgtt ctggattcta ttgaaaggta atgggagaat ggccaaaaaa 720

aaaaaaaata taggaaaggg ctttaaagta ttccgccatt ggcagggaaa gcaaaaaaaa 780

aagtgggttt tttttctcac atggtcctac tcattgggcc atataccttt ggagggttaa 840

ccaagtttaa ccagggttct atttttttgtt ttcaacacca attgcttttc tcaagggtca 900

accttaaacc caatttgtct tccgaaagaa ttttttttttt a 941

<210> SEQ ID NO 203
<211> LENGTH: 652
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 203

taattatatt atttgatttt ttttattcat gacatttatt ttatataatt ttttcttagt 60

ttggtcaaat attatcatcc ttttcattat ctcactaata aggtggattt tttttgtttg 120

acaaaatttc ttttttcaga ttggtcaaag ctaaagaaga tagaggagtt agatttatcc 180

ggcaacgaat ttaagggacc acttccctcg tcttttgtta acatgacatc tcttcgggag 240

ttggaaattt ctcataatca cttcattgga aatttcgatt ctaacattgc aagccttaca 300

tcacttgaat attttggttt tacagaaaac caatttgaag ttcctgtttc tttctcaaca 360

tttgccaatc attcaaagat caagttgatc gacggtggag gaaacagatt catattggac 420

tcacaacata gtttaccaac ttggattcca aaatttcagt tacaagagct tagtgtgtct 480

tcaacaactg aaactaagtc tcttccactc cccaattttc ttctatacca aaacagttta 540

atcagcctag acttcagtag ttggaagttg gaaggagact ttccttattg gttgttggaa 600

aacaacacaa aaatgactga agctctgttt agaaattgct ctttcactgg tg 652

<210> SEQ ID NO 204
<211> LENGTH: 699
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 204

tgcatgcctg cagcaatctc agctaaacaa gacaggtttc agcgaaaaac aaatttccat 60

-continued

tgctcacaac acacagttcg gcaaaaaagc ttcattaaac tcaaccatgc catcaccact 120

tcattctgtg tagctttgtt ttttcattca tggaaattct cagcatttca aaccccactc 180

tttgcctccc ccaaaccctc actttaaaat tcccaccaaa ccactccaaa cccacatccc 240

catttctcag aactccattt tcactctacc tatcacgctt cgccgtcata aagtttcaaa 300

cttgggcgca ttccgggcga cccagcaacc gccgcaactc cttttggaag aagctcctcc 360

gtgatcgcaa ggtaaactct aatcagattc ccaacgaccc tttctctgtt tcgggcaatg 420

gcgttgaaga gagtggtgtt ggtgatcagg gggttgacaa tgtggttgaa gttgaaaaac 480

caaagtctaa gcttttgcgt gagtctgttt tgtggaataa gttggagaat tgggctgacc 540

agtacaagag ggatgttgag tattggggtg taggatctgg tcctatattc actgtttatg 600

aagattccat tggaggtgtc aagagggtgg ttgtttatgt agaccagatt ctgaaaagaa 660

gcaaggtaaa catggctagg gagatggaga gtgggaata 699

<210> SEQ ID NO 205
<211> LENGTH: 578
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 205

aaacgtgttg aaatgaatat ttgggatctt aacaacttca ctaagatctg gaattccaaa 60

cctgtgagtc tttacttcaa cccttacttt tcatctctgc tattaattgt taacttatct 120

tcctccagtt tacctttttgt tggtgcacat tttttagtgc ttgattttac aaatccttttt 180

aacctatgca gccaactaag gataacctcg gtatatttac acctacttgt ttcacatctg 240

ctacatttct tatgaaagat gaccatcgaa aatttgttgc tggcaccaac agccatcagg 300

taaatttaat tggtagattc ttctcattct aaaataagtg aagaaatata atttttatat 360

ctaataatgc atggaatatt cctctttgat atccttgaaa aaacatgtgc tggagactat 420

tgagaaggat taataagttt ctcttaacct agaattacag agaaatggaa atgatatttt 480

tgagaatttt tttttgcaaa agaacactca agtacatgtc cttcaagtca catgagatct 540

ttcccatttt attaacaaat ataaaatgag taatatga 578

<210> SEQ ID NO 206
<211> LENGTH: 754
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 206

gagccagtat aagacatttg tggtgatcgc tctcgaccat gagaagcaga atgcaaagca 60

ttctttgaca aaaattcatc cacaagtgtt tgtaagtaat tgataacatc tttggtccaa 120

acatcagagc gagacagctg aatcttgtca gcagccccag aagaaatacc aacagaacca 180

ggtcgaacct gaaaaagcca atcataatct acaaatatta aaaaatataa agcaattcat 240

cataataggt aaatatacca acactgaagc atccctacct gattgaggta agtaaccttg 300

ataaaccagg tggccctaag caatggaaca ttattcctga taagaacctc taaaagtgat 360

gtccttttat aaccatgagg aacatgatca gccaaagagc gtaatcgctt gtgctgctga 420

gataaaccct gtaataaaat tttaactgag ttactaaaga tacattgaaa caccaagtaa 480

tgttcaaaaa gtagtattta aggattttac agccacaaca acctgtcagc atcaacaaca 540

-continued

aaaaacctaa ggccctattc ggggtggctg agttttctgt tttccgtttt aaaatgctat 600

ttcaaaatgg aaggtgttcg gctaaaatgg ttgcgagttg gatttttatc tgtttttaaa 660

acagttgtca ccccatttta taaacaataa aaataggttt tatgttttat tattttaagg 720

ttacttctat ccctacctca acgatctacg ctgc 754

<210> SEQ ID NO 207
<211> LENGTH: 798
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1)..(798)
<223> OTHER INFORMATION: unsure at all n locations; n = a, t, c, or g

<400> SEQUENCE: 207

tctatctgga gagcagaaaa ttctctccag acatgctcac ctgtggagaa tatattgcat 60

ttggagcccc ttgaggttct ctcaatatat atcattaatt tgattattga tttaagacat 120

ttatggagtg attaactgtg caagaaaata attgtatgtt taactgcctg catacatcgc 180

tatgctaatt ctgtccttca caaatctttt cacaacttgt ttgtgcatga ctctcggaaa 240

agacatgcta acatgcatat ggtgaagata agaaattaaa agaaaattgg aaaaggaaag 300

atgatatagc aatttaaata ttttttaaga tagatgtatg attgctatat cagaaaaggg 360

ttagtaaaac tagattgatg tggttgtcct ggttctcttt gatagtaaaa ttttggtatt 420

tcctttgaca catatggtgt atctttgatg gtatgtagta ataccctgga attcagcctt 480

aaattaaagc attttttttat tctctttgga aggtagatat cttccaagga gttacccttc 540

cagatgctcc aagatttgga aaggggggtt ggggggggcgg atgaattgga caggtatgaa 600

ccctactggt ttttccttcc catattaaag cacacctccc ccatgccgag gggggccctt 660

ttatacctac gcttgcgtac gtggcaagtt tattcttgta cgcccctggc cttgtagcac 720

tgtccaatcc tgggggacat tccagggttg tacagaacga attctcgtcg acgaancgtc 780

ccgtatccgg cctccacc 798

<210> SEQ ID NO 208
<211> LENGTH: 1102
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 208

gtttcgccag cttgcactgc ctgagatgaa gtaattgctg ctgcggtgct gctccggcac 60

cgccttgtgc tggtgcccgg ccaccaggta gagcaaaaga tgtcactcac tctgttcatg 120

aaaaatgggc tcaaggtcaa tgtgcatgag agggatttga gaggggttat cacaagtatt 180

aaaaaggaaa gggaggaaga tgttgatttg agaagtaacg aaagttagtg tggtgttcaa 240

tagatgaagc agagggtgtt ggaggttttt gaatgtggag acaagttcaa atgagaaaaa 300

ttcagaccct ggggctttag cttatagaac aagagaacat aatttccttt taagaaaagg 360

gtatattcag agtatttata attcttatga taaattgtgg atggattctt tttccagggt 420

cgtgggatgg atgattgctt tctcaatcca tcgttccttg tagaatcctt gcaaatattc 480

attgtattct ttatttcttg tcggttttga tgtttctatt taattttact ggtggtgaga 540

gctaaactca catttcacaa tgttgaatgt tgatgttcat aaaagaatgc cttacgtttt 600

-continued

atgaaagtat aatgatcgga tttgactctt ttgtcatata taatggatga tgcttaagtg 660

gtagtggtat actcaaaaac tgcaaaattt agctttacag ttcatctgca ttttttggtg 720

aatattcatc tgtgatttta gattctgttt ccaggatcct tgcctatgac aatgaaattg 780

aaatgcacaa attgaaccag tagtaaaagt agatatactg atgtcttttg ttaggggaca 840

ttgaatcaga aaactgtgcg accaattttc tcagccatgt atgatgaaga agcagagttg 900

gccatataac atgtatttta actttaagca taagtatgct tgagttatat aagtggacat 960

tatccaccat ctatacagaa accatttaga tcatgggaca agacatttgc aaaaggtgcc 1020

tagttaatcc aagatttcta gataaaatgt aaaggctttc agctatttga tcaaaaactt 1080

tgatggttgc tctcttcgat tt 1102

<210> SEQ ID NO 209
<211> LENGTH: 697
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 209

aagtcgcata attttgctat gaacagcttt ttgtcttaga ataatactat tttcaatcct 60

gaatataaaa aacaattatc taattcatca agatcaataa aagtaatcat attagttaat 120

ttatcataaa ttttaattat attccatgac tatccatgat tacttttcaa aagataattt 180

ttcaaccaat aagcttacct tgttttattg atagctcaat aaagacgcca cttttatggg 240

aaaatgaatg taatcattag ggataaaaaa taaatttagc aagaaaaaat tacctttttgt 300

ttctgatata tgggatggaa gtggatggaa gtagtataat gatactcatg ccattggatt 360

atctatattg cacatgctaa tttcaagcta ttggaaaatg tggaaaagag atggaattat 420

aggcatgcaa ctttaatcaa ttactatttt ctagggtgac aatgtgttta gctctaaccc 480

gaattgaaac tattaaaaaa atagatcacg atgcatgaag atagaagata tatatatcat 540

ttgagtcttt gtaatgcatg aatgctcata ttttattacc cattaaaaaa tatgggttga 600

gtggtatatt gaattttgat ttattttgtc aatcagatta gattcgaacc aactatttag 660

tataaaaaat acttttcaaa gcatttcaaa ttttcaa 697

<210> SEQ ID NO 210
<211> LENGTH: 934
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 210

ttttcacttt atctgtccct agtgtgttgt tgttattgat tggtttatgg tggtattgga 60

atgttgacca cttgtcttga cttgagtttt gactgtgtat aatggttaac tccggtctct 120

ctgttgaatg ttgttgagtt attccaagat ttgtgtgctg ctttttttttt ttttttttttt 180

ggagtggtta ggtgtaacct ttgtacttat ttttggatgc agacaaggag aaacttggct 240

aaactggagc tctaccgaaa gtttacaaac acgctcgcgg tgtctgtgtt gctgtccatt 300

gcgtggattg gctttgaggt agttcttgga aaaaatattt tgatgctcag aaatatgcaa 360

atttaggaga tttgctctat ctgtaggagt ttccaaacat tttcatttat gtatttttat 420

gcgagttgat gatgctcact aagcgttctt actgtgttca accagctata cttcaatgcc 480

actgatccat tgagtgaatt gtggcaaatt gcttggatta ttccagcttt ctggtgtctg 540

-continued

ctttcatatg ctctcttggt ggtgatatgc atcctttggg ctccatcacg gaaccctact 600

aggtacttgt tcttcccatg gtcttggggg gtgaatggta ttttttttaga gtttacctgg 660

tggttttatg cttatgtagt tagccctttt attgaaaggt ggttaatttt ttgaaattaa 720

actagttttg cattacaaag tgcttggggc tcatttgccg attttttcct tcatgcaact 780

ggattatgtc cgccacttag gggggggggta ttttgcttgt aaatatacac agcaagtgtc 840

ttcctttaaa aaagaaaaac taacccccctt actcttcttt ttattgggta gagagagaaa 900

aaacataaac aattttatgg ggggtacatt gttt 934

<210> SEQ ID NO 211
<211> LENGTH: 835
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 211

ttgcatgcct gcagacatcc tttgaaacac gctgtaaatt gagaattgta tactgattat 60

tgaatcacct ttgcagtctt acatcattgt caatgattgt accataacta tttcatttcc 120

cattacttgt aataaaagtg gctagtttat ttttgaacat atgtattaat aatagttgca 180

catgtgtgag atgatgatac atgtgcatcc tgaactcttg gaaaggtgct aaaatgagaa 240

actatctttt taaatcaggc tactttagtt ggttgaattc tgaataaagt cctctaattt 300

cttgttatga attgatatat cctctaagaa ataagaatat cgaattaaaa gttgtttaga 360

gggaaaaaga ttccccagct tttaaatgga cccagtttgt tcaaatatcc catgcaacat 420

tttactctga ccatttcact tcaacccaag taactaattg catcatagta gcatcaaata 480

cacaaacaaa aataagttaa aatcacttaa tagaattaga agaaaaaaaa atcaaaatca 540

agattctaga tattcattgc caaataaaca acgaactttg acagaagctg aaccagaaaa 600

gactaacaat aactgcttaa aataaaatca tgccagacac tgaattatgt ggtcctattg 660

attaactgaa agctccttcc gcttatatcg gaccatcact ttccccttca ctcccacaac 720

catggcattc caatcgatct ctggaaaagg tgacaccaac tccagctcaa aattcctaag 780

cagatgagtc catattgctt ttatctgcag gtcgactcta gagaggaccc gggtt 835

<210> SEQ ID NO 212
<211> LENGTH: 733
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1)..(733)
<223> OTHER INFORMATION: unsure at all n locations; n = a, t, c, or g

<400> SEQUENCE: 212

agagatcttt catgtcttca acgcccaaag actcgcactg tcacagaaac agaaacagtg 60

aaacactata aaatgctata catctacagc aaataatgaa ctatatggaa atctcctgta 120

ttttacatct atatcaaaca atacacattg aaatagcaac aatgactatt tcaaccattt 180

tttataagaa aaaattttac agataaaagg gagaaaaaaa aaattggaaa ggacaaggta 240

tttcccaaac caaggggagg tgtgggatac tgaatcttca gcttaagccc aataattgag 300

ctgaatagga taaggatatg ttaagagtat tataataaag ggctttagaa gttagttgta 360

tgtacattta taaaaatttt ttttcacaat cttttcttta tcaaaaattg agtgtgatct 420

-continued

tttcattcta aatgacagca ttactggaat attattaata ttttttttgg aaaatagatt 480

ttgaaaaact tatatgggct tggcccacat gcctttatgt acataaccta gtaatataaa 540

tatgagagtc actacacatt ggagtggagt ggatcccatt atagtttatt gacacacctc 600

tttatctttc tctctctcta ctctacatgg tatcaagagc caggtagggt ttggtgccat 660

cttcagcagc ctttctccac aaccctaaaa aactgccaaa ggaggccaac caagactgta 720

naggggggggg ggg 733

<210> SEQ ID NO 213
<211> LENGTH: 834
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1)..(834)
<223> OTHER INFORMATION: unsure at all n locations; n = a, t, c, or g

<400> SEQUENCE: 213

ctcggtnacc cggggaatcc ctctaggatc gacctgcaga aaacacaaag cctgaactca 60

gccctatcaa ggcagtgcct atgtgtaatg cagctccact gccagatatg gccagcaaaa 120

tgaatgcaat tggtgttagc accaaggctg ctccaaacca tccagttctt gcaatgtgta 180

tcttcctgca ttgtcataca acattagttg attttacgtg taatgtttgg tttcgtgtca 240

tgttctccag aatcatgtat atgtgaagca acgaagggtt gattttacgt tttggatctg 300

aattttgatc cgaatgtaca taaccaatgc atttactttg tttgccaaat ttgactgtat 360

ggtttgagaa tttttttgca ttcactttgt ttcctgtttt ctgaagttta tacaggaaaa 420

aatggaaaca gaaaatgaaa aaaagaaaaa ataaaaagtt gtttttcact gttcttgtac 480

aaaatctttа aaacatttgt ttcctgtttt ctgaagttta tactggaaaa aatggcaaca 540

gaaaatgaaa aaaataaaaa aataaaaagt tgttttcact gttcttgtac aaaatctttа 600

aaacaagaaa caaagtgaaa acagaaaatg ttttctcaaa ccaaacggtg agtgacatgc 660

ttattacctc tagaataaat cacattatgt tatgtagcaa tcactcttga atctagttga 720

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cacacatgta taaaaga 17

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ccagagtttg aatcta 16

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ctccaaccta tgattg 16

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agcctcgtct aactt 15

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cagtttccat atttc 15

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tctcgaactc attacc 16

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aatccgtcat caactt 16

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cagtatagtc agtaaaac 18

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aggagaaatt aagaaaat 18

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cagtatagtc attaaaac 18

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taggtaccat acaaaaa 17

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agaaattagg aaaataac 18

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ttgaaaataa caaagataaa t 21

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tgtttggtat gaaatta 17

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attgaaaaca acaaagat 18

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tgccactaat tatca 15

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tgctgatcta tgtttatta 19

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tgaaaagcat tagattaa 18

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tgccacaaat tat 13

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tggttgctca tcata 15

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<400> SEQUENCE: 275

tgtgaaaaac attagattaa 20

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tcgacaagaa tgggat 16

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aatgtggttg ttcatc 16

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ttattcaatg aaaatctt 18

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aatagcaaat cctaattat 19

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tggcattggt gaactc 16

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tgggacagct ttg 13

<210> SEQ ID NO 287
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aggaaataat agcatatcc 19

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ccatgaagca acaag 15

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ctggcgactg cat 13

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ccatgaagca acaag 15

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<400> SEQUENCE: 296

tcatggacaa ttggat 16

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ctggcaactg catc 14

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aggtttggaa gaggg 15

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cacttggtta atttag 16

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tgcactttgc gtggc 15

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aggtttcgaa gaggg 15

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ccttaccgat ggcg 14

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cacttcgcgt ggct 14

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ctggtttagg agaaat 16

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ccttactgat ggcggtg 17

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ctgcttctaa gatcac 16

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What is claimed is:

1. A method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant or soybean seed comprising
a. obtaining DNA from a soybean plant or soybean seed;
b. determining if alleles at a locus within maturity genomic region 1 are homozygous or heterozygous;
c. determining if alleles at a locus within maturity genomic region 2 are homozygous or heterozygous;
d. determining if alleles at a locus within maturity genomic region 3 are homozygous or heterozygous;
e. determining the allelic combination of said alleles within maturity genomic regions 1, 2, and 3; and
f. assigning a maturity group value to said soybean plant or soybean seed.

2. The method of claim **1**, wherein said determining if alleles at a locus are homozygous or heterozygous comprises detecting a polymorphism with a nucleic acid molecule comprising a sequence selected from the group consisting of SEQ ID NOs: 143-174, or complements thereof.

3. The method of claim **1** further comprising selecting multiple soybean seeds.

4. The method of claim **3**, wherein said multiple soybean seeds grow into soybean plants having indeterminate soybean plant habit.

5. The method of claim **1**, wherein said alleles at a locus within maturity genomic region 1 comprise a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 143-149, 154-155.

6. A method of establishing where a soybean plant or soybean seed should be grown by determining the allelic combination of a soybean plant comprising
a. obtaining DNA from a soybean plant or soybean seed;
b. determining if an allele within maturity genomic region 1 is homozygous or heterozygous;
c. determining if an allele within maturity genomic region 2 is homozygous or heterozygous;
d. determining the allelic combination of said alleles within maturity genomic regions 1 and 2; and
e. assigning a maturity growth value to said soybean plant or soybean seed.

7. The method of claim **6**, wherein said determining if an allele is homozygous or heterozygous comprises detecting a polymorphism selected from the group consisting of SEQ ID NOs: 143-161.

8. The method of claim **6**, wherein said soybean plant or soybean seed is obtained from a cross of an early maturity group parent soybean plant and a mid maturity parent soybean plant.

9. The method of claim **6**, wherein said early maturity group parent soybean plant is between 00.0-I.0 and said mid maturity parent soybean plant is between III.0-IV.9

10. A method of soybean plant breeding comprising
a. assaying a soybean plant for the presence of a marker sequences selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213; and
b. associating said soybean plant with a maturity group.

11. A method of soybean plant breeding comprising crossing a parent soybean plant having a desired trait with a second parent soybean plant, wherein said parent soybean plants differ in soybean plant maturity by over 10 days, comprising
a. crossing a parent soybean plant comprising a desired trait with a second parent soybean plant;
b. obtaining progeny soybean seed from said cross;
c. screening a progeny soybean seed for said trait;
d. screening a progeny soybean seed for a desired maturity group using a marker selected from the group consisting of SEQ ID NO: 143 through SEQ ID NO: 213 to determine the desired geographical growing region; and
e. selecting a progeny soybean seed containing the desired trait and desired soybean plant maturity.

12. The method of claim **11**, where said desired trait is transgenic.

13. A method of soybean plant breeding comprising
a. crossing at least two different parent soybean plants, wherein the parent soybean plants differ in soybean plant maturity by over 10 days;
b. obtaining a progeny soybean seed from said cross;
c. genotyping a progeny soybean seed of said cross with a genetic marker; and
d. selecting a soybean seed possessing a genotype for preferred maturity.

14. A method to select a soybean seed based on indeterminate or determinate growth habit comprising determining if maturity genomic region 3 is homozygous or heterozygous.

15. The method of claim **14**, wherein said maturity genomic region 3 is characterized by a G at position 433 in marker SEQ ID NO: 169.

16. A method of distributing a soybean plant based on maturity group comprising
a. obtaining DNA from a soybean plant;
b. determining if an allele within maturity genomic region 1 is homozygous or heterozygous;
c. determining if an allele within maturity genomic region 2 is homozygous or heterozygous;
d. determining if an allele within maturity genomic region 3 is homozygous or heterozygous; and
e. assigning a maturity growth value to said soybean plant; and
f. shipping said soybean plant to a preferred geographic region.

17. A method to isolate indeterminate-early maturity soybean seeds comprising
a. obtaining DNA from said soybean seed using a non-destructive method;

b. determining if an allele within maturity genomic region 1 is homozygous or heterozygous; and

c. determining if an allele within maturity genomic region 2 is homozygous or heterozygous.

18. A method to determine if a soybean plant has a maturity group of 0.0-III.9 comprising

a. obtaining DNA from said soybean seed using a non-destructive method;

b. determining if an allele within maturity genomic region 1 is homozygous or heterozygous;

c. determining if an allele within maturity genomic region 2 is homozygous or heterozygous; and

d. assigning a maturity group value for said soybean plant between 0.0-III.9.

19. The method of claim **18**, wherein maturity in said soybean plant is reached at least 5 days before a soybean plant that is homozygous dominant within maturity genomic region 1, homozygous dominant within maturity genomic region 2 and is grown under the same environmental conditions.

20. A method to determine if the maturity of a soybean plant is in a 00.0-III.0 maturity group comprising

a. determining if an allele within maturity genomic region 1 is homozygous or heterozygous;

b. determining if an allele within maturity genomic region 2 is homozygous or heterozygous; and

c. assigning a maturity group value for said soybean plant between 00.0-III.0.

21. The method of 20, further comprising selecting a soybean seed that is homozygous recessive at maturity genomic region 1 and homozygous recessive at maturity genomic region 2 and has a maturity group between 0.5-II.0.

22. The method of 20, further comprising selecting a soybean seed that is homozygous recessive at maturity genomic region 1 and heterozygous dominant at maturity genomic region 2 and has a maturity group between 1.5-II.9.

* * * * *